

XX (RICE-) RIGEL PHARM INC.
 XX
 XX Luo Y, Huang BCB, Shen M, Yu PW;
 XX WPI: 2000-205547/18.
 XX P-PSDB: AAY45042.
 XX
 PT Novel apoptotic proteins Apopt1, Apopt2 and Apopt3 and recombinant nucleic
 PT acids encoding them for use in screening modulators which is useful for
 PT diagnosis and treatment of diseases
 XX
 PS Claim 2: Fig 5: 64pp: English.
 XX
 CC The patent discloses the use of novel apoptotic proteins and related
 CC molecules involved in apoptosis modulation. Expression vectors
 CC comprising the Apopt DNA can be used to transform host cells. Apopt DNA
 CC can be administered as DNA vaccines. Apopt proteins are used to make
 CC polyclonal and monoclonal antibodies for use in immunotherapy. The
 CC proteins are useful in treating apoptosis-mediated disorders including
 CC cancer, autoimmune disorders, sustained viral infection, inappropriate
 CC cell loss and degenerative disorders. Drug candidates that affect Apopt
 CC bioactivity are identified by screening. The present sequence encodes
 CC Apopt3 protein. This was identified using RIP (receptor-interacting
 CC protein) as the bait protein employing the yeast two-hybrid screening
 CC system. Human Apopt3 is expressed in heart, liver, pancreas, placenta,
 CC and lung. Overexpression of Apopt3 inhibits TNF (tumour necrosis factor)
 CC and alpha-induced caspase activation without affecting TNFalpha-induced
 CC NFkappa B activation.
 CC
 XX Sequence 1557 BP: 397 A; 424 C; 446 G; 290 T; 0 other;
 SQ

Query Match 100.0%; Score 1557; DB 21; Length 1557;
 Best Local Similarity 100.0%; Fred. No. 0;
 Matches 1557; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 atgtctgctgaagttatctgcccagctgccccccctctgtgtgtcctcgaagaa 60.
 DB 1 atgtctgctgaagttatctgcccagctgccccccctctgtgtgtcctcgaagaa 60
 OY 61 ctggaagacagagagctcgtctcgaagacggtctcgaagagtgctcggcgcaacat 120
 DB 61 ctggaagacagagagctcgtctcgaagacggtctcgaagagtgctcggcgcaacat 120
 OY 121 aggaagctgggtctcagatctgctgagctcgaagctgaactcgaagcgatccaggag 180
 DB 121 aggaagctgggtctcagatctgctgagctcgaagctgaactcgaagcgatccaggag 180
 OY 181 gtcagagcagatgcaagctcgtatcaagaatctgtctgctcgaagaggggttaccag 240
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 DB 301 tccctgtcggggctgctgcaagctccagtgccctcggcgctcctcttcgcgcctg 360
 OY 361 ctgaaagagctgctgctggaatcttcttaactgcaagacaaagacggctctcttcgac 420
 DB 361 ctgaaagagctgctgctggaatcttcttaactgcaagacaaagacggctctcttcgac 420
 OY 421 cggagacccaagcaccacagctccctcggagccagagctgacagctgaagctggcagat 480
 DB 421 cggagacccaagcaccacagctccctcggagccagagctgacagctgaagctggcagat 480
 OY 481 ttctgacctctccacattctcaaggagctcacaagctcaagagcgagcgagggagcgag 540
 DB 481 ttctgacctctccacattctcaaggagctcacaagctcaagagcgagcgagggagcgag 540

OY 541 ggcacctgggtctacttggcccccaaaactgttttaagctaaacgggaagcctccaca 600
 DB 541 ggcacctgggtctacttggcccccaaaactgttttaagctaaacgggaagcctccaca 600
 OY 601 gccagtgaagctcacaagctcgggaatcccaatgtggcgagctgtctctggaagaagct 660
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 OY 661 gaatttcgaacgggaacacatcactgctgtatgagaagagagtgatggaagagagagag 720
 DB 661 gaatttcgaacgggaacacatcactgctgtatgagaagagagtgatggaagagagag 720
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 DB 721 tcaattgctgagctgccccagacgggcgcagaccccggtctcagaaagagctgaagag 780
 OY 781 ctaatgagctcgc 840
 DB 781 ctaatgagctcgc 840
 OY 841 ccaaaactgaatgaatcttccagatgtggagaagacaaatgaatgtctgtctccagc 900
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 OY 1081 gttcctaaataatctgc 1140
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 DB 1321 ccaaatccagtaacagggcgagacgcctgttaaatataaactgtctcgggggtgaagtc 1380
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 DB 1381 ggaagacaaacacactctgacatctgaacagacaactgtccttgcacataggggtctgga 1440
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 DB 1441 ccttcgggagcaggggaggggcttgcagacaccccccacccagtgaggttgcagaagggcct 1500
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 DB 1501 aaagatcttgaagccttgaagcagcagcaggggttggatataatcatalagcgggaataaa 1557

RESULT 2
 AAAA7702
 ID AAA47702 standard; CDNA: 1557 BP.
 ZX

XX	AAA47702.
XX	08-NOV-2000 (first entry)
XX	Kinase of death (KOD) CDS.
XX	KOD, kinase of death; programmed cell death; apoptosis; cancer;
XX	autoimmune disease; stroke; Alzheimer's disease; identification; ds.
XX	
XX	Homo sapiens.
XX	
XX	Key
XX	Location/Qualifiers
XX	1..1557
XX	CD5
XX	/tag- ^a
XX	/product- Kinase of death
XX	
XX	US6096539-A.
XX	
XX	01-AUG-2000.
XX	
XX	10-JUN-1999; 99US-0329418.
XX	
XX	10-JUN-1999; 99US-0329418.
XX	
XX	(ZENE) ZENECA LTD.
XX	
XX	Gomes BC, Prosser JC, Kasof GM;
XX	
XX	WPI: 2000-523872/47.
XX	P-PSDB: AAB01524.
XX	
XX	New nucleic acids encoding a protein activator of apoptosis for
XX	preventing, diagnosing and treating pathophysiological disorders
XX	related to apoptosis
XX	
XX	Claim 3, Columns 31-32; 32pp, English.
XX	
XX	The kinase of death (KOD) polypeptide is integral to the activation
XX	process of cellular apoptosis (programmed cell death). Apoptosis is
XX	needed to orchestrate biological maintenance of an organism during
XX	development as well as to preserve the normal function and fitness of
XX	tissues during a normal life span. Physiological conditions which
XX	result from aberrant apoptosis may be dire. Cancer and autoimmune
XX	disease may result when there is too little apoptosis as well as
XX	severe stroke damage or the neurodegeneration of Alzheimer's disease
XX	when there is too much apoptosis. The KOD polypeptide is useful for
XX	studying pathophysiological disorders related to apoptosis as well
XX	as for identifying compounds that modulate biological and/or
XX	pharmacological activity of the native mediator of apoptosis.
XX	
XX	Sequence 1557 BP; 395 A; 422 C; 448 G; 291 T; 1 other;

Query Match	99.5%	Score 1548.6;	DB 21;	Length 1557;
Best Local Similarity	99.6%	Pred. NO. 0;		
Matches 1551; Conservative	1;	Mismatches 5;	Indels 0;	Gaps 0

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QY	61	ctggagagagacccaagaaagctcgtctcggcacaagaacgggtctcggacacagtgcttcacggcgcaaacat	120
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QY	121	atgcacgacgctcacaagaattaaagagccacgcgctgcaccccccctctgtcttcacatccagaagaa	180
Db	121	atgcacgacgctcacaagaattaaagagccacgcgctgcaccccccctctgtcttcacatccagaagaa	180
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Db	181	gtccacagagccacatcggcacaagctctcggataacagaattctcgtcttcgcctctcagaaagggattatccag	240

[illegible]

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|||||
Db 1321 ccaatccagctaacagggagacgctcgttaacatacaacgctcctgggagcaagct 1380
Qy 1381 gggagacaacactactgtactatgcacacagaacactgcttgcacacatggggttgca 1440
Db 1381 gggagacaacactactgtactatgcacacagaacactgcttgcacacatggggttgca 1440
Qy 1441 ccttcgggcaaggaggggcttgcagacacccacacagtaggttcgcaagaagacccct 1500
Db 1441 ccttcgggcaaggaggggcttgcagacacccacacagtaggttcgcaagaagacccct 1500
Qy 1501 aaagaatccctgaagcttgcagacgagccacaggttgcataatcatagcgggaataa 1557
Db 1501 aaagaatccctgaagcttgcagacgagccacaggttgcataatcatagcgggaataa 1557

RESULT 3
AADI6313
ID AADI6313 standard; DNA; 1557 BP.
XX
XX AADI6313;
AC
XX 19-NOV-2001 (first entry)
DT
XX Human kinase of death (KOD) coding region.
De Human kinase of death (KOD) coding region.
XX
XX Human protein activator; apoptosis; kinase of death; KOD; therapy;
XX cytosolic; db.
OS
XX Homo sapiens.
XX
XX Key location/Qualifiers
XX CDS 1..1557
XX /tag=
XX /product= "Human kinase of death (KOD)."
XX /transcript= (pos:334..336, aa: Arg)

US6267956-B1.
PD 31-JUL-2001.
XX
XX 21-MAR-2000; 2000US-0531914.
XX
XX 10-JUN-1999; 99US-0329418.
XX
XX (ZENNE) ZENNECA LTD.
XX
XX Gomes BC, Kasof GM, Prosser JC;
XX
XX WPI; 2001-535022/59.
XX
XX P-PSDB: AAE09430.
XX
XX New human protein activator protein, useful for treating dysfunctional.
XX apoptosis conditions and in screening assays to identify agonists which
XX agonize or mimic biological and/or pharmacological activity -
XX
XX Disclosure: Column 31-32; 31pp; English.
XX
XX The invention relates to human protein activator of apoptosis and
XX methods to identify compounds that modulate the biological and/or
XX pharmacological activity of the activator and hence regulate
XX apoptosis. The nucleic acid and amino acid sequences of the kinase
XX of death (KOD) are useful for identifying compounds that modulate
XX the biological and/or pharmacological activity of a native mediator
XX of apoptosis, for treating dysfunctional apoptosis conditions, in
XX screening assays to identify agonists which agonize or mimic
XX biological and/or pharmacological activity, induce production of or
XX prolong the biological half-life of the molecule in vivo or in vitro.
XX The present DNA sequence is the coding region of human KOD protein
XX activator of apoptosis.
XX
XX Sequence 1557 BP: 395 A; 422 C; 448 G; 291 T; 1 other:

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Query Match 99.5%; Score 1548.6; DB 22; Length 1557;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 1551; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

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Db 1 atctcgtcgtcgaagtatcatgagccagcagctgccccccccccttgggtgctacatcagga 60
Qy 61 ctggagaaacagagagctcgttcggaagaaggggttcggcaatgttccgggcgaagaat 120
Db 61 ctggagaaacagagagctcgttcggaagaaggggttcggcaatgttccgggcgaagaat 120
Qy 61 ctggagaaacagagagctcgttcggaagaaggggttcggcaatgttccgggcgaagaat 120
Db 61 ctggagaaacagagagctcgttcggaagaaggggttcggcaatgttccgggcgaagaat 120
Qy 121 aggaagctggggtcagcagctcgggttcaagaatcgttaaacctcgaagcgatccagggag 180
Db 121 aggaagctggggtcagcagctcgggttcaagaatcgttaaacctcgaagcgatccagggag 180
Qy 181 gtcagaagccatctgcaagctcgtggaataacgaattcgttgcgcctcgaagaagggttctcag 240
Db 181 gtcagaagccatctgcaagctcgtggaataacgaattcgttgcgcctcgaagaagggttctcag 240
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Db 241 aagtgaaactggggaacagaatcccaagccgctcgtgtgaactaattcatagagaagc 300
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Db 301 tccctcgtcgggtcgtcagctccagctgcccctcggccctcgtcgtccttgcgcgctg 360
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Db 361 ctgaaagaagatgggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 420
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Db 421 cgggaccccaagccatcccaagctcctgcggagcccaagctcgaatcgaatcgaatcgaat 480
Qy 481 ttgtcgtcgtcgaatcctcaagagagctcgaatcgaatcgaatcgaatcgaatcgaatcga 540
Db 481 ttgtcgtcgtcgaatcctcaagagagctcgaatcgaatcgaatcgaatcgaatcgaatcga 540
Qy 541 ggcacccctgggtcacttggccccaagaactgttgttaacgttaaacccggaagccctccca 600
Db 541 ggcacccctgggtcacttggccccaagaactgttgttaacgttaaacccggaagccctccca 600
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Db 601 gcaagtgaactcagctcagctcgggttccctaaatgtggcagtgctgtcgtgaagaagaat 660
Qy 661 gacttgcacacgaacacacacacacacacacacacacacacacacacacacacacacacac 720
Db 661 gacttgcacacgaacacacacacacacacacacacacacacacacacacacacacacacac 720
Qy 721 tcaatgtcgtcagctcagctcagctcagctcagctcagctcagctcagctcagctcagctc 780
Db 721 tcaatgtcgtcagctcagctcagctcagctcagctcagctcagctcagctcagctcagctc 780
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Db 841 ccaaaactatgaatcctcgaagctcgtcgaagctcgtcgaagctcgtcgaagctcgtcgaag 900
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Qy 961 ggcagaagagagcagaataatgagctttagagaacacatagaataacacagacacacac 1020
Db 961 ggcagaagagagcagaataatgagctttagagaacacatagaataacacagacacacac 1020

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OY 1021 aatgatactgcttctcagtcagtcgtaaaactgaactgaactgagggagcctccagctct 1080
DB 1021 aatgatactgcttctcagtcagtcgtaaaactgaactgaactgagggagcctccagctct 1080
OY 1081 gtctctaaataatgctccgagcttcaacaaagagagcgagggcagaaagagagcgagcttca 1140
DB 1081 gtctctaaataatgctccgagcttcaacaaagagagcgagggcagaaagagagcgagcttca 1140
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DB 1381 gggagacacacactactctgacatacgcacagacacacacacacacacacacacacacacacac 1440
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DB 1501 aagagatcctgaaagcctgagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 1557

RESULT 4
AAK94599 standard: cDNA, 1871 BP.
ID AAK94599
AC AAK94599:
XX
XX 06-NOV-2001 (first entry)
XX
XX Human full-length cDNA, SEQ ID NO: 3541.
XX
XX Human: full length cDNA; cDNA synthesis; oligo-capping; ss.
XX
XX Homo sapiens.
XX
XX EP1130094-A2.
XX
XX 05-SEP-2001.
XX
XX 07-JUL-2000; 2000EP-0114089.
XX
XX 08-JUL-1999; 99JP-0194486.
XX 11-JAN-2000; 2000JP-0118774.
XX 02-MAY-2000; 2000JP-0183765.
XX
XX (HELI-) HELIX RES INST.
XX
XX Oka T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y,
XX Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;
XX WPI; 2001-534255/58.
XX P-PSDB; AAM93664.
XX
XX 830 Primers useful for synthesizing full length cDNA clones and their
XX use in genetic manipulation -
XX
XX Claim 8: SEQ ID NO 3541; 1380bp + sequence listing: English.

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XX
CC The invention relates to primers for synthesizing full length cDNA
CC clones. 830 cDNA molecules encoding a human protein have been
CC isolated and nucleotide sequences of 5'- and 3'-ends of the cDNA
CC molecules have been determined. Primers for synthesizing the full length
CC cDNA are useful for clarifying the function of the protein encoded by
CC the cDNA. The full length clones were obtained by construction of full
CC length enriched cDNA libraries that were synthesised by the oligo-capping
CC method. The primers enable the production of the full length cDNA easily
CC without any special methods. The present sequence is a full length
CC human cDNA of the invention.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in CD-ROM format directly from EPO.
XX
SO Sequence 1871 BP; 474 A; 528 C; 516 G; 353 T; 0 other;

Query Match 98.8%; Score 1538; DB 22; Length 1871;
Best Local Similarity 99.8%; Pred. No. 0; Mismatches 5; Indels 1; Gaps 1;
Matches 1552; Conservative 0;

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DB 165 atgtctgctcagatgatactgagccagcagctgagccagccagccctgtgtctcagagaa 224
OY 61 ctgagagaaacagagagcctcgtcagcagagagcgttcagcagagcttcagcagcagcagcagc 120
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DB 285 aggaatgagggctcagatgtgtcgtcagagatcgttaaacctcgaagcagcagcagcagcagc 344
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OY 601 gccagtgagctcagagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 660
DB 765 gccagtgagctcagagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 824
OY 661 gagttgcaaacagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 720
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DB 885 tcattgctgagctgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 944

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QY 781 ctaatgacgtctgtgagagcgtgagccagagagacccctctccagagatccca 840
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 QY 841 ccaaaacgtatgagagcgtctccagatggtgagagacatagatgctgtctccag 900
 DB 1005 ccaaaacgtatgagagcgtctccagatggtgagagacatagatgctgtctccag 1064
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 QY 961 ggcacagagagagagacatgagatggtgagagacatagatgctgtctccag 1020
 DB 1125 ggcacagagagagagacatgagatggtgagagacatagatgctgtctccag 1184
 QY 1021 aatgagatgctgtctccagatggtgagagacatagatgctgtctccagatgca 1080
 DB 1185 aatgagatgctgtctccagatggtgagagacatagatgctgtctccagatgca 1244
 QY 1081 gttctt-aaaaaagcccgagccttaccagagagagagagagagagagagatcc 1139
 DB 1245 gttctt-aaaaaagcccgagccttaccagagagagagagagagagagagatcc 1304
 QY 1140 acagagccttgagagagagacatctctccagatggtgagagacatctccagatc 1199
 DB 1305 acagagccttgagagagagacatctctccagatggtgagagacatctccagatc 1364
 QY 1200 gacctaacttcag 1259
 DB 1365 gacctaacttcag 1424
 QY 1260 acccag 1319
 DB 1425 acccag 1484
 QY 1320 gccaaatccag 1379
 DB 1485 gccaaatccag 1544
 QY 1380 tggagagac 1439
 DB 1545 tggagagac 1604
 QY 1440 accctcgag 1499
 DB 1605 accctcgag 1664
 QY 1500 taagaatcctgagagccttgagagagagagagagagagagagagagagagag 1557
 DB 1665 taagaatcctgagagccttgagagagagagagagagagagagagagagagag 1722
 RESULT 5
 AAA47701 standard; cDNA: 1873 BP.
 ID AAA47701;
 AC AAA47701;
 AT 08-NOV-2000 (first entry)
 DE Kinase of death (KOD) coding sequence.
 DX KOD: kinase of death; programmed cell death; apoptosis; cancer;
 KW autoimmune disease; stroke; Alzheimer's disease; identification; ds.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT CDS 165..1724
 FT /*tag= a
 FT /product= Kinase of death
 XX

PN DS6096539-A.
 XX 01-AUG-2000.
 PD 10-JUN-1999; 99US-0329418.
 PF 10-JUN-1999; 99US-0329418.
 PR 10-JUN-1999; 99US-0329418.
 XX (ZENEC) ZENEC LTD.
 PA Gomes BC, Prosser JC, Kasof GM;
 PI WPI: 2000-523872/47.
 DR P-PSDS: AAB01524.
 XX
 PT New nucleic acids encoding a protein activator of apoptosis for
 PT preventing, diagnosing and treating pathophysiological disorders
 PT related to apoptosis
 PS Claim 9; Columns 29-32; 32pp; English.
 CC The kinase of death (KOD) polypeptide is integral to the activation
 CC of cellular apoptosis (programmed cell death). Apoptosis is
 CC needed to orchestrate biological maintenance of an organism during
 CC development as well as to preserve the normal function and fitness of
 CC tissues during a normal life span. Physiological conditions which
 CC result from aberrant apoptosis may be dire. Cancer and autoimmune
 CC disease may result when there is too little apoptosis as well as
 CC severe stroke damage or the neurodegeneration of Alzheimer's disease
 CC when there is too much apoptosis. The KOD polypeptide is useful for
 CC studying pathophysiological disorders related to apoptosis as well
 CC as for identifying compounds that modulate biological and/or
 CC pharmacological activity of the native mediator of apoptosis.
 CC
 SQ Sequence 1873 BP; 471 A; 531 C; 518 G; 353 T; 0 other;
 Query Match 98.0%; Score 1526.4; DB 21; Length 1873;
 Best Local Similarity 99.1%; Pred. No. 0;
 Matches 1546; Conservative 0; Mismatches 11; Indels 3; Gaps 1;
 QY 1 atgtcgtgctcaagttaatgagcagcgtgagccgcccctgtgtctccagagaa 60
 DB 165 atgtcgtgctcaagttaatgagcagcgtgagccgcccctgtgtctccagagaa 224
 QY 61 ctgagagacagagcgtctgagcagagagagagagagagagagagagagagagag 120
 DB 225 ctgagagacagagcgtctgagcagagagagagagagagagagagagagagag 284
 QY 121 agagagtgagagcgtgagcgtgagcgtgagcgtgagcgtgagcgtgagcgtgag 180
 DB 285 agagagtgagagcgtgagcgtgagcgtgagcgtgagcgtgagcgtgagcgtgag 344
 QY 181 gtcaaggtcagagcgtgagcgtgagcgtgagcgtgagcgtgagcgtgagcgtgag 240
 DB 345 gtcaaggtcagagcgtgagcgtgagcgtgagcgtgagcgtgagcgtgagcgtgag 404
 QY 241 aaggtc--gaactgagcagacacacacacacacacacacacacacacacacacac 297
 DB 405 aaggtcggcggtcagcagacacacacacacacacacacacacacacacacacac 464
 QY 298 ggtcctcgtgagcgtgagcgtgagcgtgagcgtgagcgtgagcgtgagcgtgag 357
 DB 465 ggtcctcgtgagcgtgagcgtgagcgtgagcgtgagcgtgagcgtgagcgtgag 524
 QY 358 ctgctgaaagagagtggtgagtggttcttaccgtgagcagacacacacacacac 417
 DB 525 ctgctgaaagagagtggtgagtggttcttaccgtgagcagacacacacacacac 584
 QY 418 caccggagcctcagagcagcagcgtcgtcagcagcagcagcagcagcagcagcagc 477
 DB 585 caccggagcctcagagcagcagcgtcgtcagcagcagcagcagcagcagcagcagc 644

QY 478 gatttggccgtccacatttcaggagcctcagtcaggagacagggctccggggagcca 537
 |||||||
 Db 645 gatttggccgtccacatttcaggagcctcagtcaggagacagggctccggggagcca 704
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 QY 538 ggggggacccctggggtacttggcccgaaactgttggtaagctaaacgggaagccctcc 597
 |||||||
 Db 705 ggggggacccctggggtacttggcccgaaactgttggtaagctaaacgggaagccctcc 764
 |||||||
 QY 598 aagacagatgacgtctacagcttcggggtcctaaatgctgggagctgcttgcgtgaaagaa 657
 |||||||
 Db 765 aagacagatgacgtctacagcttcggggtcctaaatgctgggagctgcttgcgtgaaagaa 824
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 Db 825 gttgagttgcccac 884
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 |||||||
 Db 885 ccttcaattggcctgagacgtcccccacacacacacacacacacacacacacacacac 944
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 Db 945 gaggtaatgacgtctgagagcagtgagcccaagagacagacccctcctccaggaatgac 1004
 |||||||
 QY 838 ctac 897
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 Db 1005 ctac 1064
 |||||||
 QY 898 acggttaaaagatcttcctgctcagcctcaagacagacagatagagatcttcctacccag 957
 |||||||
 Db 1065 acggttaaaagatcttcctgctcagcctcaagacagacagatagagatcttcctacccag 1124
 |||||||
 QY 958 tcaaggccaaggagagagagagagatgagctttagagagagacacacacacacacacac 1017
 |||||||
 Db 1125 tcaaggccaaggagagagagatgagctttagagagagacacacacacacacacacac 1184
 |||||||
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 |||||||
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 |||||||
 QY 1078 tctgtctctaaanaaaatgcccagaccttaccagaaggagacagggccaagaagagac 1137
 |||||||
 Db 1245 tctgtctctaaanaaaatgcccagaccttaccagaaggagacagggccaagaagagac 1304
 |||||||
 QY 1138 ccacaaagcctggagacagcagcagcactcttcagatctgagtgcccaacacacacacac 1197
 |||||||
 Db 1305 ccacaaagcctggagacagcagcagcactcttcagatctgagtgcccaacacacacacac 1364
 |||||||
 QY 1198 gggacctcaactcttcagaaacacagatgcccacactcaactcagacacacacacac 1257
 |||||||
 Db 1365 gggacctcaactcttcagaaacacagatgcccacactcaactcagacacacacacac 1424
 |||||||
 QY 1258 ggaaccgagagagatcagaggggctgagagacagagacatgaactgctcctcagagac 1317
 |||||||
 Db 1425 ggaaccgagagagatcagaggggctgagagacagagacatgaactgctcctcagagac 1484
 |||||||
 QY 1318 gggccaacatccagatcaacagggcgacgctcgtttacaatatacactgctcctggggta 1377
 |||||||
 Db 1485 gggccaacatccagatcaacagggcgacgctcgtttacaatatacactgctcctggggta 1544
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 QY 1378 gttgagagacaaacactctgactaagcacaacagacacacacacacacacacacacac 1437
 |||||||
 Db 1545 gttgagagacaaacactctgactaagcacaacagacacacacacacacacacacacac 1604
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 QY 1438 ggaacctgggagagagagagggcttgcagacaccccccacacacacacacacacacac 1497
 |||||||
 Db 1605 ggaacctgggagagagaggggcttgcagacaccccccacacacacacacacacacac 1664
 |||||||
 QY 1498 ccttaagaatcccgaaagcctggagagagcagacaggttggtaatacacaacagcggaataa 1557
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 Db 1665 ccttaagaatcccgaaagcctggagagagcagacaggttggtaatacacaacagcggaataa 1724
 |||||||

RESULT 6
 AAD16312
 ID AAD16312 standard; cDNA: 1873 BP.
 XX
 AC AAD16312;
 XX
 DF 19-NOV-2001 (first entry)
 XX
 DE Human kinase of death (KOD) cDNA.
 XX
 KW Human: protein activator; apoptosis; kinase of death; KOD; therapy;
 KW cytosolic; ss.
 XX
 OS Homo sapiens.
 XX
 FT Key Location/Qualifiers
 FT CDS 165..1724
 FT /tag= a
 FT /product= "Human kinase of death (KOD)"
 FT /transl_except= (pos:411..472, aa: Asn-Trp-Asp)
 FT
 XX US6267956-21.
 XX
 PD 31-JUL-2001.
 PD
 XX 21-MAR-2000: 2000US-0531914.
 XX
 PR 10-JUN-1999: 99US-0329418.
 PR
 XX (ZENRE) ZENRECA LTD.
 XX
 PI Gomes BC, Rasof GM, Prosser JC,
 XX
 DR MP1: 2001-535022/59.
 DR P-PSDB: AAE09430.
 XX
 PT New human protein activator protein, useful for treating dysfunctional
 PT apoptosis conditions and in screening assays to identify agonists which
 PT agonize or mimic biological and/or pharmacological activity -
 XX
 XX Example 3; Column 29-32; 31pp; English.
 PS
 CC The invention relates to human protein activator of apoptosis and
 CC methods to identify compounds that modulate the biological and/or
 CC pharmacological activity of the activator and hence regulate
 CC apoptosis. The nucleic acid and amino acid sequences of the kinase
 CC of death (KOD) are useful for identifying compounds that modulate
 CC the biological and/or pharmacological activity of a native mediator
 CC of apoptosis, for treating dysfunctional apoptosis conditions, in
 CC screening assays to identify agonists which agonize or mimic
 CC biological and/or pharmacological activity, induce production of or
 CC prolong the biological half-life of the molecule in vivo or in vitro.
 CC The present sequence is a cDNA encoding human KOD protein activator
 CC
 CC
 XX
 SO Sequence 1873 BP: 471 A: 531 C: 518 G: 353 T: 0 other:
 Query Match 98.04; Score 1526.4; DB 22; Length 1873;
 Best Local Similarity 99.11; Pred. No. 0;
 Matches 1546; Conservative 0; Mismatches 11; Indels 3; Gaps 1;
 QY 1 atctctgctcgaattatggcccgagctgccccccctctgtgctcctcagagaa 60
 |||||||
 Db 165 atctctgctcgaattatggcccgagctgccccccctctgtgctcctcagagaa 224
 |||||||
 QY 61 ctggagaaacacagagacgtctgagcaagaggggttgcagagttcttcggcgcaaat 120
 |||||||
 Db 225 ctggagaaacacagagacgtctgagcaagaggggttgcagagttcttcggcgcaaat 284
 |||||||
 QY 121 aggaagttgggtcagatgctggcggtcagaatcgttaaacctcgaagcgatccaggag 180
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 Db 285 aggaagttgggtcagatgctggcggtcagaatcgttaaacctcgaagcgatccaggag 344
 |||||||


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|||||
Db 1 ggaagaaacagagagctcgcgcgaagagcggtctcgccaggtgtcccggtgcaacacaaag 60
Oy 123 gaaatgagagagagagagctcgcgcgaagagcggtctcgccaggtgtcccggtgcaacacaaag 182
Db 61 gaaatgagagagagagagctcgcgcgaagagcggtctcgccaggtgtcccggtgcaacacaaag 120
Oy 183 caaagagagagagagagctcgcgcgaagagcggtctcgccaggtgtcccggtgcaacacaaag 242
Db 121 caaagagagagagagagctcgcgcgaagagcggtctcgccaggtgtcccggtgcaacacaaag 180
Oy 243 ggtgagagagagagagagctcgcgcgaagagcggtctcgccaggtgtcccggtgcaacacaaag 302
Db 181 ggtgagagagagagagagctcgcgcgaagagcggtctcgccaggtgtcccggtgcaacacaaag 240
Oy 303 cctgagagagagagagagctcgcgcgaagagcggtctcgccaggtgtcccggtgcaacacaaag 362
Db 241 cctgagagagagagagagctcgcgcgaagagcggtctcgccaggtgtcccggtgcaacacaaag 300
Oy 363 gaaagagagagagagagctcgcgcgaagagcggtctcgccaggtgtcccggtgcaacacaaag 422
Db 301 gaaagagagagagagagctcgcgcgaagagcggtctcgccaggtgtcccggtgcaacacaaag 360
Oy 423 ggaagagagagagagagctcgcgcgaagagcggtctcgccaggtgtcccggtgcaacacaaag 482
Db 361 ggaagagagagagagagctcgcgcgaagagcggtctcgccaggtgtcccggtgcaacacaaag 420
Oy 483 tggagagagagagagagctcgcgcgaagagcggtctcgccaggtgtcccggtgcaacacaaag 542
Db 421 tggagagagagagagagctcgcgcgaagagcggtctcgccaggtgtcccggtgcaacacaaag 480
Oy 543 caagagagagagagagagctcgcgcgaagagcggtctcgccaggtgtcccggtgcaacacaaag 602
Db 481 caagagagagagagagagctcgcgcgaagagcggtctcgccaggtgtcccggtgcaacacaaag 540
Oy 603 cagagagagagagagagctcgcgcgaagagcggtctcgccaggtgtcccggtgcaacacaaag 662
Db 541 cagagagagagagagagctcgcgcgaagagcggtctcgccaggtgtcccggtgcaacacaaag 600
Oy 663 gttgagagagagagagagctcgcgcgaagagcggtctcgccaggtgtcccggtgcaacacaaag 722
Db 601 gttgagagagagagagagctcgcgcgaagagcggtctcgccaggtgtcccggtgcaacacaaag 660
Oy 723 attgagagagagagagagctcgcgcgaagagcggtctcgccaggtgtcccggtgcaacacaaag 782
Db 661 attgagagagagagagagctcgcgcgaagagcggtctcgccaggtgtcccggtgcaacacaaag 720
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Db 721 aatgagagagagagagagctcgcgcgaagagcggtctcgccaggtgtcccggtgcaacacaaag 780
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Db 781 aaaaagagagagagagagctcgcgcgaagagcggtctcgccaggtgtcccggtgcaacacaaag 840
Oy 903 aaaaagagagagagagagctcgcgcgaagagcggtctcgccaggtgtcccggtgcaacacaaag 962
Db 841 aaaaagagagagagagagctcgcgcgaagagcggtctcgccaggtgtcccggtgcaacacaaag 900
Oy 963 ccaagagagagagagagagctcgcgcgaagagcggtctcgccaggtgtcccggtgcaacacaaag 1022
Db 901 ccaagagagagagagagagctcgcgcgaagagcggtctcgccaggtgtcccggtgcaacacaaag 960
Oy 1023 tgaatgagagagagagagagctcgcgcgaagagcggtctcgccaggtgtcccggtgcaacacaaag 1082
Db 961 tgaatgagagagagagagagctcgcgcgaagagcggtctcgccaggtgtcccggtgcaacacaaag 1020
Oy 1083 tcttaaaaaagagagagagagctcgcgcgaagagcggtctcgccaggtgtcccggtgcaacacaaag 1142
Db 1021 tcttaaaaaagagagagagagctcgcgcgaagagcggtctcgccaggtgtcccggtgcaacacaaag 1080
Oy 1143 agccagagagagagagagagctcgcgcgaagagcggtctcgccaggtgtcccggtgcaacacaaag 1202

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Db 1081 agcctgagagagagagagctcgcgcgaagagcggtctcgccaggtgtcccggtgcaacacaaag 1140
Oy 1203 ctcagagagagagagagagctcgcgcgaagagcggtctcgccaggtgtcccggtgcaacacaaag 1262
Db 1141 ctcagagagagagagagagctcgcgcgaagagcggtctcgccaggtgtcccggtgcaacacaaag 1200
Oy 1263 ccgagagagagagagagagctcgcgcgaagagcggtctcgccaggtgtcccggtgcaacacaaag 1322
Db 1201 ccgagagagagagagagagctcgcgcgaagagcggtctcgccaggtgtcccggtgcaacacaaag 1260
Oy 1323 aatcagagagagagagagagctcgcgcgaagagcggtctcgccaggtgtcccggtgcaacacaaag 1382
Db 1261 aatcagagagagagagagagctcgcgcgaagagcggtctcgccaggtgtcccggtgcaacacaaag 1320
Oy 1383 agagagagagagagagagagctcgcgcgaagagcggtctcgccaggtgtcccggtgcaacacaaag 1442
Db 1321 agagagagagagagagagagctcgcgcgaagagcggtctcgccaggtgtcccggtgcaacacaaag 1380
Oy 1443 ttcgagagagagagagagagctcgcgcgaagagcggtctcgccaggtgtcccggtgcaacacaaag 1502
Db 1381 ttcgagagagagagagagagctcgcgcgaagagcggtctcgccaggtgtcccggtgcaacacaaag 1440
Oy 1503 agatcagagagagagagagagctcgcgcgaagagcggtctcgccaggtgtcccggtgcaacacaaag 1557
Db 1441 agatcagagagagagagagagctcgcgcgaagagcggtctcgccaggtgtcccggtgcaacacaaag 1495

RESULT 8
AAAT5675
ID AAAT5675 standard; DNA: 2140 BP.
XX
AC AAAT5675;
XX
DT 22-JAN-2001 (first entry)
XX
DB DNA encoding a human regulator of intracellular phosphorylation.
XX
NM Human; intracellular phosphorylation regulator; RHP; stroke; myeloma;
NM neurological disorder; Parkinson's disease; demyelinating disease;
NM meningitis; developmental disorder; neuromuscular disorder; cancer;
NM myasthenia gravis; cell proliferative disorder; actinic keratosis;
NM arteriosclerosis; atherosclerosis; leukemia; melanoma; bronchitis;
NM autoimmune disorder; inflammatory disorder; Addison's disease;
NM acquired immunodeficiency disease; allergy; diabetes mellitus;
NM rheumatoid arthritis; microbial infection; trauma; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 395..1852
FT /tag="a
FT /product="regulator of intracellular phosphorylation"
XX
XX MO20005332-A2.
XX
XX 21-SEP-2000.
XX
XX 17-MAR-2000; 2000MO-US07277.
XX
XX 18-MAR-1999; 9905-0125593.
XX 20-MAR-1999; 9905-0135049.
XX 09-JUL-1999; 9905-0143188.
XX
XX (INCY-) INCYTE PHARM INC.
XX
XX Bandman O, Tang YT, Yue H, Killman JL, Baughn MR, Azimzal Y;
XX Lu DM, Au-Young J;
XX
XX MPI: 2000-602121/57.
XX P-PDB: AAB16658.
XX
XX Novel human intracellular phosphorylation regulator polypeptides and
XX polynucleotides for diagnosis, prevention and treatment of

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AA30546
ID AAF30546 standard; cDNA; 1437 BP.
XX
XX AAF30546;
XX
XX 29-MAY-2001 (first entry)
XX
XX Rat RIP-3-like death-associated kinase (R3DAK) cDNA.
XX
XX RIP-3-like death-associated kinase; R3DAK; rat; antibacterial;
XX virucide; protozoacide; cardiant; antiinflammatory; vasotropic;
XX antidiabetic; antitumor; analgesic; immunosuppressive;
XX antihypertensive; hepatotropic; cytoskeletal; nocotropic;
XX anticonvulsant; hepatotropic; antiallergic; uropathic;
XX dermatological; osteoporosis; antiparkinsonian; antipsychotic; neuroprotective;
XX pulmonary; hormonal; apoptosis; gene therapy; vaccine; 88.
XX
XX Rattus sp.
XX
XX WO200119990-A1.
XX
XX 22-MAR-2001.
XX
XX 15-SEP-2000; 2000MO-US25201.
XX
XX 17-SEP-1999; 99US-0154422.
XX
XX (IMMUNEX CORP.
XX
XX Vlcra CD, Bird TA:
XX
XX WPI: 2001-244803/25.
XX
XX P-PSDB: AAB20345.
XX
XX New isolated RIP-3-like death-associated kinase polypeptide for
XX treating multiple sclerosis, Parkinson's disease, Sjogren's disease,
XX infections, tumours, cardiovascular and lymphoproliferative disorders
XX
XX Claim 5: Page 56-57; 63pp; English.
XX
XX The present sequence is that of the coding region of cDNA encoding
XX rat RIP-3-like death-associated kinase (R3DAK, see AAB20345), a
XX member of the RIP3 family, which is known to be involved in
XX apoptosis. The cDNA was obtained from a rat dermal papilla cell
XX library. The invention provides R3DAK polypeptides and a
XX polynucleotide, expression vectors, recombinant host cells, and
XX methods of producing a recombinant R3DAK polypeptide, as well as
XX antibodies, a method of designing an R3DAK inhibitor on the basis
XX of the 3-dimensional structure of a R3DAK polypeptide, a method of
XX identifying compounds that alter R3DAK kinase activity, and for
XX using such compounds. R3DAK, its fragments, variants, agonists,
XX agonists, antibodies and binding partners are useful for treating:
XX bacterial, viral or protozoal infections; cardiovascular disorders such
XX as myocardial infarction, heart failure, or vasculitis; solid tumours;
XX chronic pain; endocrine system disorders such as diabetes;
XX hypothyroidism and thyroiditis, including Hashimoto's thyroiditis;
XX gastrointestinal diseases such as Crohn's disease and ulcers;
XX genitourinary system disorders such as glomerulonephritis; hematologic
XX and oncologic disorders such as cancer; lymphoproliferative disorders
XX such as Hodgkin's disease; hereditary conditions such as Gaucher's and
XX Huntington's disease; liver disorders such as hepatitis; non-arthritis
XX medical conditions of the bones and joints; pulmonary disorders such as
XX cystic fibrosis; allergies; rheumatic disorders such as systemic lupus
XX erythematosus, gout, osteoarthritis, Reiter's disease;
XX graft-versus-host disease; female reproductive system disorders; and
XX diseases such as multiple sclerosis, Parkinson's disease, Sjogren's
XX disease. R3DAK is useful for effecting bodily characteristics,
XX biohythme or cardiac cycles or rhythms; effecting the fertility of
XX male or female subjects; effecting the metabolism, catabolism
XX anabolism, processing, utilization, storage or elimination of dietary
XX fat, lipid, polypeptide, carbohydrates, vitamins, minerals, cofactors
XX or other nutritional factors or component(s); effecting behavioural

CC characteristics; providing analgesic effects or other pain reducing
CC effects; promoting differentiation and growth of embryonic stem cells
CC in lineages other than haematopoietic lineages; hormonal or endocrine
CC activity; treatment of hyperproliferative disorders;
CC immunoglobulin-like activity; and the ability to act as an antigen in a
CC vaccine composition. Nucleic acids encoding R3DAK are useful for
CC diagnostic purposes, for expressing recombinant polypeptide for
CC analysis, characterisation or therapeutic use, as markers for tissues
CC in which the corresponding polypeptide is preferentially expressed,
CC to compare with endogenous DNA sequences in patients to identify
CC potential genetic disorders; as an antigen to raise anti-DNA
CC antibodies or elicit another immune response; and for gene therapy.
XX
XX Sequence 1437 BP; 368 A; 359 C; 399 G; 311 T; 0 other:
SO
Query Match 43.3%; Score 673.6; DB 22; Length 1437;
Best Local Similarity 69.4%; Pred. No. 9.5e-175;
Matches 1024; Conservative 0; Mismatches 404; Indels 48; Gaps 6;
OY 1 ATGCTGCTCAAGTATGAGCCAGCGTCCCGC---CCCTGCTGCTCATCGAG 57
DB 1 ATGCTGCTCAAGTATGAGTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGAG 60
OY 58 GAATGAG 117
DB 61 GAATGAG 120
OY 118 CATAG 177
DB 121 CATAG 180
OY 178 GAGTCAAG 237
DB 181 GAGTCAAG 240
OY 238 GAGTCAAG 297
DB 241 GAGTCAAG 300
OY 298 GAGTCAAG 357
DB 301 GAGTCAAG 360
OY 358 GAGTCAAG 417
DB 361 GAGTCAAG 420
OY 418 GAGTCAAG 477
DB 421 GAGTCAAG 480
OY 478 GAGTCAAG 531
DB 481 GAGTCAAG 540
OY 532 GAGTCAAG 591
DB 541 GAGTCAAG 597
OY 592 GAGTCAAG 651
DB 598 GAGTCAAG 657
OY 652 GAGTCAAG 711
DB 658 GAGTCAAG 717
OY 712 GAGTCAAG 771
DB 718 GAGTCAAG 777
OY 772 GAGTCAAG 831

```
Db 778 ctgaaaggggttaatgacgcatctgtgagtcctgagccaaagagcgacatctctccaa 837
      ||||| ||||| || ||||| ||||| ||||| ||||| ||||| ||||| |||||
Oy 832 gaatgccaccacaaacatgataagctctccagatggtgagagaacaataatgactgcct 891
      || || ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 838 gactgtgaatacaaaacaaataatcttacaatcctgtgtacaggaagataagatctgct 897
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Oy 892 gtctccaaagataaagattctctgtctcaagctcaagagcagcaataagagattctctac 951
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 898 gtctccaaagataaagattctctgtctcaagctcaagagcagcaataagagattctctac 957
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Oy 952 ccagagatcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 1011
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 958 agagagatcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 1008
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Oy 1012 caactctgtaatgataatgataatgataatgataatgataatgataatgataatgata 1071
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1009 -----gttaagaaatgtctgacccgcctgcatctgagagagccc 1047
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Oy 1072 ccagatctgttcttaaaaaatgcgcgagccttaacaaagagcagcagcagcagcagcag 1131
      || || ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1048 tctgatactagctctgaaagactcaagaatcttactgagagag---agagaaagaaagca 1104
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Oy 1132 caggttccaaagcctgagcagcagcagcagcagcagcagcagcagcagcagcagcag 1191
      || || ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1105 tcaattggtcactgacacacacagcagcagcagcagcagcagcagcagcagcagcagc 1164
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Oy 1192 actccagagacactcaacttcaagaaacagatgcccagcctcaactcagctgagacaca 1251
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1165 attccacatacttcaactcctcagagcagcagcagcagcagcagcagcagcagcagcag 1224
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Oy 1252 agtcttgaaaccccgaggaatacagaggtgctgagagaagaacagcagcagcagcagc 1311
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1225 ggtcctgaccccaaaagaaatcagagagatggaagaacagcagcagcagcagcagcag 1284
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Oy 1312 acccggagacaaatcagtaacagagcagcagcagcagcagcagcagcagcagcagcag 1371
      || || ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1285 aac---gacccaacacacatgacaggtctacagtctcttcttaaacacatgctctgaa 1341
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Oy 1372 gtgcaagtttgagaaacaaatacttgaactgaacaaacagcagcagcagcagcagcag 1431
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1342 gtgcaagatttgacacacacacatgcatgtcgtacaaacagcagcagcagcagcagcag 1401
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Oy 1432 ggtctgcagacctcggcgaagggagggctgcag 1467
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1402 gagccagacaggttcgcagagggtagggctgtag 1437
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 10
AAK57466
ID AAK57466 standard; cDNA; 939 BP.
AC AAK57466;
AT 06-NOV-2001 (first entry)
DT XX
EX Human immune/haematopoietic antigen encoding cDNA SEQ ID NO:2526.
DE XX
KW Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
KN cytotoxic; gene therapy; vaccine; metastasis; ss.
OS Homo sapiens.
XX MOJ00157182-A2.
PM 09-AUG-2001.
PD 17-JAN-2001; 2001MO-US01354.
PF 31-JAN-2000; 2000US-0179065.
PR 04-FEB-2000; 2000US-0180628.
PR 24-FEB-2000; 2000US-0184664.
PR 02-MAR-2000; 2000US-0186350.
PR 16-MAR-2000; 2000US-0189874.
PR 17-MAR-2000; 2000US-0190076.
PR 18-APR-2000; 2000US-0198123.
PR 19-MAY-2000; 2000US-0205515.
PR 07-JUN-2000; 2000US-0209466.
PR 28-JUN-2000; 2000US-0214886.
PR 30-JUN-2000; 2000US-0215135.
PR 07-JUL-2000; 2000US-0216647.
PR 07-JUL-2000; 2000US-0216880.
PR 11-JUL-2000; 2000US-0217487.
PR 11-JUL-2000; 2000US-0217496.
PR 14-JUL-2000; 2000US-0218290.
PR 16-JUL-2000; 2000US-0220963.
PR 16-JUL-2000; 2000US-0220964.
PR 16-JUL-2000; 2000US-0224518.
PR 14-AUG-2000; 2000US-0224519.
PR 14-AUG-2000; 2000US-0225213.
PR 14-AUG-2000; 2000US-0225214.
PR 14-AUG-2000; 2000US-0225266.
PR 14-AUG-2000; 2000US-0225267.
PR 14-AUG-2000; 2000US-0225268.
PR 14-AUG-2000; 2000US-0225270.
PR 14-AUG-2000; 2000US-0225271.
PR 14-AUG-2000; 2000US-0225275.
PR 14-AUG-2000; 2000US-0225757.
PR 14-AUG-2000; 2000US-0225758.
PR 14-AUG-2000; 2000US-0225759.
PR 18-AUG-2000; 2000US-0226279.
PR 22-AUG-2000; 2000US-0226681.
PR 22-AUG-2000; 2000US-0226686.
PR 22-AUG-2000; 2000US-0227182.
PR 23-AUG-2000; 2000US-0227009.
PR 30-AUG-2000; 2000US-0228924.
PR 01-SEP-2000; 2000US-0229287.
PR 01-SEP-2000; 2000US-0229343.
PR 01-SEP-2000; 2000US-0229344.
PR 01-SEP-2000; 2000US-0229345.
PR 05-SEP-2000; 2000US-0229509.
PR 05-SEP-2000; 2000US-0229513.
PR 06-SEP-2000; 2000US-0230437.
PR 06-SEP-2000; 2000US-0230438.
PR 08-SEP-2000; 2000US-0231242.
PR 08-SEP-2000; 2000US-0231243.
PR 08-SEP-2000; 2000US-0231244.
PR 08-SEP-2000; 2000US-0231413.
PR 08-SEP-2000; 2000US-0231414.
PR 08-SEP-2000; 2000US-0232080.
PR 08-SEP-2000; 2000US-0232081.
PR 12-SEP-2000; 2000US-0231968.
PR 14-SEP-2000; 2000US-0232397.
PR 14-SEP-2000; 2000US-0232398.
PR 14-SEP-2000; 2000US-0232399.
PR 14-SEP-2000; 2000US-0232400.
PR 14-SEP-2000; 2000US-0232401.
PR 14-SEP-2000; 2000US-0233053.
PR 14-SEP-2000; 2000US-0233054.
PR 14-SEP-2000; 2000US-0233055.
PR 14-SEP-2000; 2000US-0234223.
PR 21-SEP-2000; 2000US-0234274.
PR 21-SEP-2000; 2000US-0234997.
PR 25-SEP-2000; 2000US-0234998.
PR 26-SEP-2000; 2000US-0235484.
PR 27-SEP-2000; 2000US-0235834.
PR 27-SEP-2000; 2000US-0235836.
PR 29-SEP-2000; 2000US-0236327.
PR 29-SEP-2000; 2000US-0236367.
PR 29-SEP-2000; 2000US-0236368.
PR 29-SEP-2000; 2000US-0236369.
PR 29-SEP-2000; 2000US-0236370.
PR 02-OCT-2000; 2000US-0236802.
PR 02-OCT-2000; 2000US-0237037.
PR 02-OCT-2000; 2000US-0237038.
PR 02-OCT-2000; 2000US-0237039.
PR 02-OCT-2000; 2000US-0237040.
```


[illegible]

CC	AAK65951 to AAK6702 encode the human immune/hematopoietic antigen (I)
CC	amino acid sequences given in AAK62110 to AAK61951. (I) have cytosolic
CC	activity, and can be used in gene therapy and vaccine production. (I)
CC	protein and polynucleotides may be used in the prevention, diagnosis and
CC	treatment of diseases associated with inappropriate (I) expression. For
CC	example, they may be used to treat disorders associated with decreased
CC	expression by rectifying mutations or deletions in a patient's genome
CC	that affect the activity of (I) by expressing inactive proteins or to
CC	supplement the patient's own production of (I). Additionally, (I)
CC	polynucleotides may be used to produce the secreted (I), by inserting
CC	the nucleic acids into a host cell and culturing the cell to express the
CC	protein. (I) proteins and polynucleotides may be used to prevent,
CC	diagnose and treat immune/hematopoietic-related diseases, especially
CC	cancers and cancer metastases of haematopoietic-derived cells. AAK64703
CC	to AAK6794 represent human Immune/Hematopoietic antigen genomic
CC	sequences from the present invention. AAK51942 to AAK51950 and AAK82169
CC	represent sequences used in the exemplification of the present invention..
XX	
XX	
SQ	Sequence 939 BP; 263 A; 271 C; 231 G; 174 T; 0 other;
	Query Match 42.2%; Score 656.4; DB 22; Length 939;
	Best Local Similarity 99.8%; Pred. No. 4.2e-110;
	Matches 657; Conservative 0; Mismatches 1; Indels 0; Gaps 0
OY	900 ggttaaaagattctcgtctccagtccaagaagcgacaatagagattttctaccagaagtc 959
DB	128 ggttaaaagattctcgtctccagtccaagaagcgacaatagagattttctaccagaagtc 187
OY	960 agtgcgaaggaggacagaagaatggatggtcttcaggagacccaataaaaacagacacctg 1019
DB	188 agtgcgaaggaggacagaagaatggatggtcttcaggagacccaataaaaacagacacctg 247
OY	1020 taatgatgtcatggtcttcgtatggtgtttaaacaaactgatatcttgaggagctcccaagtc 1079
DB	248 taatgatgtcatggtcttcgtatggtgtttaaacaaactgatatcttgaggagctcccaagtc 307
OY	1080 tgtctctaataanaatgcccagaccttaccagaaggagcgacagcaaaagagagagagttcc 1139
DB	308 tgtctctaataanaatgcccagaccttaccagaaggagcgacagcaaaagagagagagttcc 367
OY	1140 acaaagctctgagacagagcacatcttcagatctcgaatggccccaaacctcccaagctccaga 1199
DB	368 acaaagctctgagacagagcacatcttcagatctcgaatggccccaaacctcccaagctccaga 427
OY	1200 gaacttaaatcttcngaaaaacagatggcccgccctccctccaaacttgaaacaccaagtcctgg 1259
DB	428 gaacttaaatcttcngaaaaacagatggcccgccctccctccaaacttgaaacaccaagtcctgg 487
OY	1260 accccgaggggaatcagaggggcttgaaagacaagcatgnaactggtctctgacagagaccctgga 1319
DB	488 accccgaggggaatcagaggggcttgaaagacaagcatgnaactggtctctgacagagaccctgga 547
OY	1320 gccaaatctcagaaataoagagcgacagctctgtatacaataaacaatgctctgaggttgcaagt 1379
DB	548 gccaaatctcagaaataoagagcgacagctctgtatacaataaacaatgctctgaggttgcaagt 607
OY	1380 tggtagagcaaaactactactgtgactcttgaaagaagaacactgctctggcccaacttgagggtctgg 1439
DB	608 tggtagagcaaaactactactgtgactcttgaaagaagaacactgctctggcccaacttgagggtctgg 667
OY	1440 acctctggcgaaggagggaggtcttgacagacaccccccacagtagtgtctgcaagaagagccc 1499
DB	668 acctctggcgaaggagggaggtcttgacagacaccccccacagtagtgtctgcaagaagagagccc 727
OY	1500 taagaagctcttaagaagccctggagcgagcgacaaaggtttggtataacaatagcggagaataa 1557
DB	728 taagaagctcttaagaagccctggagcgagcgacaaaggtttggtataacaatagcggagaataa 785
RESULT 11	
AA527210	
ID	AA527210 standard; cDNA; 960 bp.

PR 17-NOV-2000; 2000US-0249297.
 PR 17-NOV-2000; 2000US-0249299.
 PR 17-NOV-2000; 2000US-0249300.
 PR 01-DEC-2000; 2000US-0250160.
 PR 01-DEC-2000; 2000US-0250191.
 PR 05-DEC-2000; 2000US-0251030.
 PR 05-DEC-2000; 2000US-0251988.
 PR 05-DEC-2000; 2000US-0256719.
 PR 06-DEC-2000; 2000US-0251479.
 PR 08-DEC-2000; 2000US-0251856.
 PR 08-DEC-2000; 2000US-0251868.
 PR 08-DEC-2000; 2000US-0251889.
 PR 08-DEC-2000; 2000US-0251989.
 PR 11-DEC-2000; 2000US-0251990.
 PR 05-JAN-2001; 2001US-0259678.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 PI Rosen CA, Barash SC, Ruben SM;
 XX
 DR MPI: 2001-465460/50.
 DR P-PSDB: MA017293.
 XX
 PT Novel polypeptides useful for diagnosing, treating, preventing and/or
 PT prognosing disorders related to the proteins, including cancers, immune
 PT disorders and neuronal disorders -
 XX
 PS Claim 1; SEQ ID No 245; 880bp; English.
 XX
 CC The invention relates to novel isolated polypeptides (I), and
 CC polynucleotides (II). (I), (II) and the antibody to (I) are useful for
 CC diagnosing, preventing and treating diseases including immune system
 CC disorders (e.g. congenital and acquired immunodeficiencies, autoimmune
 CC disorders (e.g. rheumatoid arthritis), inflammatory conditions, organ
 CC transplant rejections and graft versus host disease, infectious diseases
 CC (e.g. hepatitis C), bleeding disorders, haemoglobin abnormalities and
 CC other blood-related disorders (sickle cell anemia), myeloproliferative
 CC disorders, primary haematopoietic disorders, hyperproliferative
 CC disorders (e.g. Gaucher's disease and cancer), neurodegenerative
 CC disorders (e.g. Alzheimer's disease, Parkinson's disease), chromosomal
 CC abnormalities (Down syndrome), ischaemic injury (e.g. stroke), renal
 CC disorders (e.g. glomerulonephritis), cardiovascular disorders
 CC (e.g. arrhythmia), respiratory disorders, dermatological disorders, in
 CC wound healing, epithelial cell proliferation, endocrine disorders (e.g.
 CC Addison's disease), reproductive system disorders, gastrointestinal
 CC disorder (inflammatory disorders), liver disorders (cirrhosis),
 CC as stimulators of B-cell responsiveness to pathogens, activators of
 CC T-cells, to induce higher affinity antibodies, and as a means to induce
 CC tumour proliferation in pathologies e.g. acquired immune deficiency
 CC syndrome (AIDS). MAS26576-MAS27850 represent novel signal transduction
 CC pathway protein coding sequences and PCR primers of the invention.
 CC
 XX
 Query Match 40.4%; Score 629; DB 22; Length 960;
 Best Local Similarity 95.8%; Pred. No. 1.4e-162;
 Matches 761; Conservative 1; Mismatches 19; Indels 13; Gaps 11;
 XX
 OY 1 atgtctgctgataaattatgtcgcacggcgccccccttggttcacatggagaa 60
 Db 165 atgtctgctgataaattatgtcgcacggcgccccccttggttcacatggagaa 224
 OY 61 ctggaagacacagagagctcgtcgcacagcggttcgcgacagtgctccggcgacacat 120
 Db 225 ctggaagacacagagagctcgtcgcacagcggttcgcgacagtgctccggcgacacat 284
 OY 121 aggaagctgggctacagatgtcgctcaagatcgtataactcgaagcgatcccgagag 180
 Db 285 aggaagctgggctacagatgtcgctcaagatcgtataactcgaagcgatcccgagag 344
 OY 181 gtcaagagcgaatgacagctgataaagattcgtctcgcctcgaaggggttatcgag 240
 Db 345 gtcaagagcgaatgacagctgataaagattcgtctcgcctcgaaggggttatcgag 404

OY 241 aaggtgactggagaccagaatcccaagccggtctctgtgtactaaattcatctgagagacggc 300
 Db 405 aaggtgactggagaccagaatcccaagccggtctctgtgtactaaattcatctgagagacggc 464
 OY 301 tccctctggagctgtctgaatctccagctgcctcggcctccttcgtccgctcgt 360
 Db 455 tccctctggagctgtctgaatctccagctgcctcggcctccttcgtccgctcgt 524
 OY 361 ctgaagaagatgtgtcttggaatgtttacatccagcagcaaacacggctctctcagac 420
 Db 525 ctgaagaagatgtgtcttggaatgtttacatccagcagcaaacacggctctctcagac 584
 OY 421 cgggacctcaagcaccatcccaacgctcgtccgagcagagctcagctcagagat 480
 Db 585 cgggacctcaagcaccatcccaacgctcgtccgagcagagctcagctcagagat 643
 OY 481 ttggcctgtccacattccaggggtccacagtccagggagcaggggtccgggagacagg 540
 Db 644 ttggcctgtccacattccaggggtccacagtccagggagcaggggtccgggagacagg 702
 OY 541 ggcacccctgggtactctggcccgagacctgtttgttaacgtataaccggagagctccaca 600
 Db 703 ggcacccctgggtactctggcccgagacctgttgg-taacgtataaccggagagctccaca 761
 OY 601 ggcagctgagctc-tacagcttc-ggagctcctaatgt-gggcagctgtctcgtgagagaa 657
 Db 762 ggcagctgagctccttcagctcctcgggatcctaatgttggggcaggtgtctcgtgagagaa 821
 OY 658 gttagatctgcacacggaaccatcactcgttgaagagagatgtgcacagcgagacagg 717
 Db 822 -ttgagctgcacacggaaccatcactcgttgaagagagca-ttgcacaaagcgagacagg 879
 OY 718 ccttccttgctgagctgcgcc--aagccgggctgagatcccggtta--gaagagact 773
 Db 880 -ccttccttgctgagctgcgcccaagcgggcttgnaatnccgcttaanaagactt 938
 OY 774 gaagagctaatatgc 787
 Db 939 aagagctaatatgc 952
 XX
 RESULT 12
 AAK92320
 ID AAK92320 standard; cDNA: 665 BP.
 XX
 AC AAK92320;
 XX
 DT 06-NOV-2001 (first entry)
 XX
 DE Human cDNA 5'-end sequence, SEQ ID NO: 780.
 XX
 RT Human: full length cDNA; cDNA synthesis; oligo-capping; ss.
 XX
 OS Homo sapiens.
 XX
 PN EP1130094-A2.
 XX
 FD 05-SEP-2001.
 XX
 PF 07-JUL-2000; 2000EP-0114089.
 XX
 PR 08-JUL-1999; 99JP-0194486.
 PR 11-JAN-2000; 2000JP-0118774.
 PR 02-MAY-2000; 2000JP-0183765.
 XX
 PA (HELI-) HELIX RES INST.
 XX
 PI Oka T, Nishikawa T, Isogai T, Hayashi K, Iahli S, Kawai Y;
 PI Nakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuka T, Koga H;
 DR MPI: 2001-524255/58.
 XX

830 Primers useful for synthesizing full length cDNA clones and their use in genetic manipulation -

Claim 2: SEQ ID NO 780: 1380bp + sequence listing; English.

The invention relates to primers for synthesizing full length cDNA clones. 830 cDNA molecules encoding a human protein have been isolated and nucleotide sequences of 5'- and 3'-ends of the cDNA molecules have been determined. Primers for synthesizing the full length cDNA are useful for clarifying the function of the protein encoded by the cDNA. The full length clones were obtained by construction of full length enriched cDNA libraries that were synthesised by the oligo-capping method. The primers enable the production of the full length cDNA easily without any special methods. The present sequence is the nucleotide sequence of the 5'-end of a cDNA provided in the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in CD-ROM format directly from EPO.

Sequence 665 BP: 147 A; 194 C; 190 G; 130 T; 4 other:

Query Match 29.2%; Score 454.8; DB 22; Length 665;
Best Local Similarity 96.2%; Pred. No. 8.5e-115;
Matches 485; Conservative 0; Mismatches 16; Indels 3; Gaps 2;

```

OY 1 atgtcgtcgtaaggtatgagccagcggtgccccccctgtgtgtcattcagagaa 60
    |||||||
DB 165 atgtcgtcgtaaggtatgagccagcggtgccccccctgtgtgtcattcagagaa 224
OY 61 ctggagaaacccagagcggtcgtgcaagagagaggttcgagacagtttcggggcgacaat 120
    |||||||
DB 225 ctggagaaacccagagcggtcgtgcaagagagaggttcgagacagtttcggggcgacaat 284
OY 121 aggaagatggggtcgtgcaagatcggtcgaagatcgtaacctgaagcgatcatcaggag 180
    |||||||
DB 285 aggaagatggggtcgtgcaagatcggtcgaagatcgtaacctgaagcgatcatcaggag 344
OY 181 gtcaagagcagtgcaagatctgtgatacgaattcgtgttcgcgcctgaaggggttaccag 240
    |||||||
DB 345 gtcaagagcagtgcaagatctgtgatacgaattcgtgttcgcgcctgaaggggttaccag 404
OY 241 aaggtgaacttgagacaaagatcccaagcgggtcgtgtaacttaatttcagaaagacgc 300
    |||||||
DB 405 aaggtgaacttgagacaaagatcccaagcgggtcgtgtaacttaatttcagaaagacgc 464
OY 301 tccctgtcggtggtcgtgcaagtcaccagtcgcctcgccctggcgcgtcccttgcgcgctg 360
    |||||||
DB 465 tccctgtcggtggtcgtgcaagtcaccagtcgcctcgccctggcgcgtcccttgcgcgctg 523
OY 361 ctgaagaagatggtgctggtggttttaccctgacagacagaaacccgggtgctccctgac 420
    |||||||
DB 524 ctgaagaagatggtgctggtggttttaccctgacagacagaaacccgggtgctccctgac 583
OY 421 cgggaaacctcaagacatccaaagtcctcgccgagaccagaaagctcacagctgagcagat 480
    |||||||
DB 584 cgggaaacctcaagacatccaaagtcctcgccgagaccagaaagctcacagctgagcagatc 641
OY 481 ttgggcctgtccacattcaggga 504
    |||||||
DB 642 ttctgtcgtccacattcaggga 665

```

RESULT 13
AAK93863
ID AAK93863 standard; cDNA: 665 BP.
XX
XX AAK93863:
AC
XX 06-NOV-2001 (first entry)
BT
XX Human cDNA clone representative sequence, SEQ ID NO: 2323.
DE
XX Human; full length cDNA; cDNA synthesis; oligo-capping; ss.
KW

XX Homo sapiens.

XX EP130094-A2.

XX 05-SEP-2001.

XX 07-JUL-2000; 2000EP-0114089.

XX 08-JUL-1999; 99JP-0194486.

XX 11-JAN-2000; 2000JP-0118774.

XX 02-MAY-2000; 2000JP-0183765.

XX (HELI-) HELIX RES INST.

XX Oka T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y;

XX Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;

XX WPI; 2001-524255/58.

XX 830 Primers useful for synthesizing full length cDNA clones and their use in genetic manipulation -

Example 11: SEQ ID NO 2323; 1380bp + sequence listing; English.

The invention relates to primers for synthesizing full length cDNA clones. 830 cDNA molecules encoding a human protein have been isolated and nucleotide sequences of 5'- and 3'-ends of the cDNA molecules have been determined. Primers for synthesizing the full length cDNA are useful for clarifying the function of the protein encoded by the cDNA. The full length clones were obtained by construction of full length enriched cDNA libraries that were synthesised by the oligo-capping method. The primers enable the production of the full length cDNA easily without any special methods. The present sequence was used in representative sequence to identify the clone.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in CD-ROM format directly from EPO.

Sequence 665 BP: 147 A; 194 C; 190 G; 130 T; 4 other:

Query Match 29.2%; Score 454.8; DB 22; Length 665;
Best Local Similarity 96.2%; Pred. No. 8.5e-115;
Matches 485; Conservative 0; Mismatches 16; Indels 3; Gaps 2;

```

OY 1 atgtcgtcgtaaggtatgagccagcggtgccccccctgtgtgtcattcagagaa 60
    |||||||
DB 165 atgtcgtcgtaaggtatgagccagcggtgccccccctgtgtgtcattcagagaa 224
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OY 481 ttgggcctgtccacattcaggga 504
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 DB 546 GATTTCTATCCAGAGTCAGCCCAAGGAGGCC--AAATGAGGCGCTTAGGAGAACCA 489
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Search completed: August 13, 2002, 21:16:07
 Job time: 4049 sec

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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: August 13, 2002, 20:00:12 ; Search time 1587.62 Seconds

(without alignments)
13236.643 Million cell updates/sec

Title: US-09-762-491-5

Perfect score: 1557

Sequence: 1 atgcgcgcgcacgaattatg.....ataatcatatgcgggaataaa 1557

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 13736207 seqs, 6748477542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 08

Maximum Match 1008
Listing first 45 summaries.

Database :

EST.*
1: em_estdb.*
2: em_esthum.*
3: em_estlin.*
4: em_estnu.*
5: em_estov.*
6: em_estpl.*
7: em_estro.*
8: em_hic.*
9: gb_estl.*
10: gb_estl2.*
11: gb_hic.*
12: gb_gss.*
13: em_gss_hum.*
14: em_gss_inv.*
15: em_gss_pin.*
16: em_gss_vrt.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	684.4	44.0	929	10	BIT70357
2	675	43.4	897	10	BIT838468
3	659.4	42.4	1026	10	BIT819557
4	615.8	39.6	922	10	BIT823411
5	600.4	38.6	630	9	AW959157
6	561.8	36.1	1855	11	AK012177
7	464	29.8	643	10	BE001916
8	463.4	29.8	758	9	AL601137
9	445.6	28.6	616	10	BIT83736
10	445.8	27.3	440	9	AA227673
11	393.8	25.3	432	10	BF359285
12	388.4	24.9	906	10	BF359285
13	382	24.4	451	10	BF359287
14	380.4	24.5	414	10	BF359303
15	359.6	23.1	388	10	BF359467
16	359	23.1	983	10	BG253717
17	352	22.6	377	10	BF359290

C 18	348.4	22.4	359	10	BF359469	BF359469 RC6-ET008
C 19	347.2	22.3	532	10	BF196648	BF196648 7m3e01.x
C 20	342.4	22.0	600	10	BF1985826	BF1985826 3152-49 M
C 21	335	21.5	500	10	BF063009	BF063009 7h74a06.x
C 22	327.2	21.0	782	10	BF1911862	BF1911862 603063648
C 23	325.4	20.9	821	9	AM106218	AM106218 um24a06.y
C 24	321	20.6	471	9	AM009940	AM009940 w889f02.x
C 25	320	20.6	378	10	BF359468	BF359468 RC6-ET008
C 26	312	20.0	452	9	AI394293	AI394293 t909f09.x
C 27	311.8	20.0	444	9	AA491391	AA491391 aa65c08.x
C 28	308	19.8	372	10	BF354781	BF354781 RC4-HT078
C 29	300.8	19.3	576	10	BI341529	BI341529 368991 MA
C 30	299.4	19.2	421	10	BM106587	BM106587 510498 MA
C 31	299	19.2	451	9	AI082857	AI082857 ov24e09.y
C 32	298.2	19.2	344	10	BE832097	BE832097 PM2-ET007
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C 34	293.6	18.7	860	10	BI413255	BI413255 60288395
C 35	291.6	18.7	453	9	AM875071	AM875071 RC6-ET000
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C 38	270.2	17.4	568	10	BF080096	BF080096 230854 MA
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C 40	258.6	16.6	273	9	AA361942	AA361942 EST71276
C 41	257	16.5	430	10	BE676675	BE676675 7f34b06.x
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C 44	253.2	16.3	287	10	BF359473	BF359473 RC6-ET008

ALIGNMENTS

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DEFINITION 60305627F1 NIH_MGC_122 Homo sapiens cDNA clone IMAGE:5205618 5',
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BIT70357
ACCESSION BIT70357.1 GI:15761935
VERSION BIT70357
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 929)
AUTHORS NIH-MGC http://mgi.ncl.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Email: cgaups-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L1AM1515 row: 1 column: 19
High quality sequence stop: 870.
Location/Qualifiers
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/clone="IMAGE:5205618"
/clone_id="NIH_MGC_122"
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/note="Organ: pooled lung and spleen; Vector: pCMV-SPORT6;
Site: 1: Not; Site 2: EcoRV (destroyed); RNA source
anonymous pool of 24 week female lung, 16 week female
spleen, and 20-22 week male spleens. Library is oligo-dT
primed and directionally cloned (EcoRV site is destroyed
upon cloning). Average insert size 1.4 kb, insert size

FEATURES

source

[illegible]

Matches	783;	Conservative	0;	Mismatches	37;	Indels	12;	Gaps	9;
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Dh	148	atgtccgtgcctcaagtattatggtccacgcagtcgccccccttggtgtctcatcagaa	207						
Oy	61	ctgtagaaccaagaagctctgctcgcaaaagcgggtctcgtgcaagctgtctccggcgcaaat	120						
Dh	208	cttgagaaacacgaagctctcgtccgcaaaagccgggttcggcacaagtggtccggcgcaaat	267						
Oy	121	aggaagaaggagagctacagatgtggcagctcaagaatcttaactctgaagagagataccaaagag	180						
Dh	268	aggaagaaggagagctacagatgtggcagctcaagaatcttaactctgaagagagataccaaagag	327						
Oy	181	gtcaaaagcatalgccaagctctggaataaagaattcgtgtcgcctagaagagggttatcag	240						
Dh	328	gtcmaagccctatggcgaagctctggaataaagaattcgtgtcgcctagaagagggttatcag	387						
Oy	241	aaggtctgaactctggaacaaagatcccaagccggctctgtgtgaactcaatcatctggaagacgc	300						
Dh	388	aaggtctgaactctggaacaaagatcccaagccggctctgtgtgaactcaatcatctggaagacgc	447						
Oy	301	tcctctgctcaggggtctgtctcaggtctcccaaggtccctctggccctctggtcctcttcgcctct	360						
Dh	448	tcctctgctcaggggtctgtctcaggtctcccaaggtccctctggccctctggtcctcttcgcctct	507						
Oy	361	ctgaagaagaatgtgtctctggaatgttttaactctgaacgaacacccgggtgtcctctcag	420						
Dh	508	ctgaagaagaatgtgtctctggaatgttttaactctgaacgaacacccgggtgtcctctcag	567						
Oy	421	cggaacctcaagcatalcacaagctcctctgcggaacccaagagctgtcagctcagctcagat	480						
Dh	568	cggaacctcaagcatalcacaagctcctctgcggaacccaagagctgtcagctcagctcagat	627						
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Dh	687	ggcaacctgggtctactctggtcccaagaactgtctcttaagtgtaaacccggaagagccttcaca	745						
Oy	601	ggcagtagcgtctcacaagctctcggatctcctaaatctgggcagtgctctctcgaagaaagaa	658						
Dh	746	ggcagtagcgtctcacaagctctcggatctcctaaatctgggcagtgctctctcgaagaaagaa	805						
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KEYWORDS	EST.								
SOURCE	human.								
ORGANISM	Homo sapiens								
REFERENCE	1	Mammalia: Eutheria; Primates; Catarrhini; Hominidae; Homo.							
AUTHORS	NIH-NCBI	http://mgi.nci.nih.gov/.							

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: c9apbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (ULNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/ULNL at:
http://image.llnl.gov
Plate: LLM11454 Row: a Column: 13
High quality sequence start: 2
High quality sequence stop: 785.
Location/Qualifiers

FEATURES
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/lab_host="DH10B"
/note="Origin: pooled brain, lung, testis; Vector: PCMV-SPORE; Site_1: NotI; Site_2: EcoRV (destroyed); RNA source anonymous pool of 6 male brains, age range 23-27; 1 male lung, age 27; and 1 male testis, age 69. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.8 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (In vitro). Research Genetics tracking code 021. Note: this is a NTH_MGC Library."

BASE COUNT 206 a 269 c 270 g 177 t
ORIGIN

Query Match 39.6%; Score 615.8; DB 10; Length 922;
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Matches 712; Conservative 0; Mismatches 27; Indels 10; Gaps 7;
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RESULT 5
LOCUS AN959157 630 bp mRNA linear EST 01-JUN-2000
DEFINITION EST371227 MAGE resequences, MAGE Homo sapiens cDNA, mRNA sequence.
ACCESSION AN959157
VERSION AN959157.1 GI:8148841
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SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 630)
Hogde, P., Qi, R., Abernathy, K., Dharap, S., Gaspar, R., Gay, C., Holt, I.E., Saeed, A.I., Sharov, V., Lee, N.H., Yeaman, T.J. and Quackenbush, J.
Assessment of gene expression patterns in a model of colon tumor metastasis using a 19,200 element cDNA microarray
Published (2000)
Contact: John Quackenbush
The Institute for Genomic Research
7712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 3528
Fax: 301 838 0208
Email: johnqu@tigr.org
Plate: 130

FEATURES
source
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_id="MAGE resequences, MAGE"
/note="Vector: pBluescriptKm"

BASE COUNT 180 a 170 c 164 g 116 t
ORIGIN

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Matches 616; Conservative 0; Mismatches 11; Indels 1; Gaps 1;
849 tgatgaagcttctcagaatggtgagaaacatataatgagctgtcttcccaagataaagga 908
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|||||
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DB 241 AAATGCCCAAGCCTTACCAAGAGGAGGACACAAAGAGAGAGGTTCCACAAACCTG 300

OY 1149 gacacgagcagcctctcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 1208

DB 301 GACGAGCAGCAGCTTTCAGATTCATGAGCCCAACCTCCAGAGCTCCAGAGACCTCAAC 360

OY 1209 tttcagaacacagatgcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 1268

DB 361 TTTTGAAGAACAGATGCTCCAGCCCTTACCACTGGAACACCAAGTCTCTGAGCCGAG 420

OY 1269 gaacacagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 1328

DB 421 GAATCAGAGCGGCTGAGAGCAAGAGGATGATGCTGCTGAGAGAGCCCGAGCAAAATCC 480

OY 1329 agtaacagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 1388

DB 481 AGTAAACAGGCGAGCCCTGCTTAACTATTAACATGCTGCGGTGCAAGTTGAGACAA 540

OY 1389 caactacttgactactgacacacagacacacacacacacacacacacacacacacacacacac 1447

DB 541 CAATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 600

OY 1448 gcaagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 1477

DB 601 GCCAGGGGAGGGGTGTCACACCCGCC 630

RESULT 6

AK012177 1853 bp mRNA linear RIKEN 19-JAN-2002

LOCUS AK012177

DEFINITION Mus musculus 10 days embryo whole body cDNA, RIKEN full-length

PROTEIN 3, full insert sequence.

ACCESSION AK012177.1 GI:12848761

VERSION AK012177.1

KEYWORDS RNC, CAP, trapper.

SOURCE Mus musculus (strain: C57BL/6J) 10 days embryo cDNA to mRNA, clone: 11b:RIKEN full-length enriched mouse cDNA library

ORGANISM Mus musculus

REFERENCE 1 (sites) Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

AUTHORS Carninci, P. and Hayashizaki, Y.

JOURNAL High efficiency full-length cDNA cloning

REFERENCE 2 (sites) Meth. Enzymol. 303, 19-44 (1999)

AUTHORS Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M., and Hayashizaki, Y.

TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes

JOURNAL Genome Res. 10 (10), 1617-1630 (2000)

REFERENCE 3 (sites) Shibata, K., Itoh, M., Aizawa, K., Nagasaka, S., Sasaki, N., Carninci, P., Kono, H., Akiyama, J., Nishikawa, K., Kikunishi, T., Teishiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishikawa, T., Barada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujisawa, S., Inoue, K., Togawa, Y., Iwata, M., Ohara, E., Kashiwagi, K., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuda, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A., and Hayashizaki, Y.

TITLE RIKEN integrated sequence analysis (RISA) system-384 format

JOURNAL sequencing pipeline with 384 multiplexed sequencer

REFERENCE 4 (sites) Genome Res. 10 (11), 1757-1771 (2000)

DB 1107881

REFERENCE 4 (sites) The RIKEN Genome Exploration Research Group Phase II team and the FANTOM Consortium.

TITLE Functional annotation of a full-length mouse cDNA collection

JOURNAL Nature 409, 685-690 (2001)

REFERENCE 5 (bases 1 to 1853)

AUTHORS Adachi, J., Aizawa, K., Akahira, S., Akimura, T., Aono, H., Arai, A., Arakawa, T., Baidarrelli, R., Bono, H., Brownstein, M., Bull, C., Carninci, P., Fukuda, S., Fukunishi, Y., Furuno, M., Hanagaki, T., Hara, A., Hayatsu, N., Hill, D., Hiramoto, K., Hirooka, F., Hori, F., Hume, D., Inokuni, K., Ishii, Y., Itoh, M., Iwata, M., Kashiwagi, T., Kato, H., Kawai, J., Kojima, Y., Kono, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Nishikawa, K., Nomura, K., Numazaki, R., Ohno, M., Okazaki, Y., Oikawa, T., Owa, C., Quackenbush, J., Saito, H., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Schiraldi, L., Shibata, K., Shibata, Y., Shinagawa, A., Shirekhi, T., Sobabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Tanaka, T., Teijima, Y., Toy, T., Yamamoto, T., Yamamoto, T., Yasunishi, A., Yoshida, K., Yoshino, M., Muramatsu, M. and Hayashizaki, Y.

TITLE Direct Submission

JOURNAL Submitted (10-JUN-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-rs@gs.riken.go.jp, URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)

COMMENT Please visit our web site (<http://genome.gsc.riken.go.jp/>) for further details.

FEATURES

source location/Qualifiers

1. 1853

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/strain="C57BL/6J"

/db_xref="MGI:1910134"

/db_xref="taxon:10090"

/clone="2610528K09"

/clone_11b="RIKEN full-length enriched mouse cDNA library"

/dev_stage="10 days embryo"

1. 1853

/note="data source: SPT, source key: 090210, evidence: ISS similar to RECEPTOR INTERACTING PROTEIN 3"

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Best Local Similarity 66.3% Pred. No. 4.7e-131;

Matches 996; Conservative 0; Mismatches 432; Indels 75; Gaps 10;

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DB 242 CGGTCTCTCTGCTGAGCGGTGAAGAACTGAAGAACTGAGTGTGCTGAAGAGAGGT 301

OY 95 tcgagc 154

DB 302 TCGAGCTGCTTTCGCGGACACACAGAACTGAAGAACTGAGTGTGCTGAAGAGGT 361

OY 155 taaactcgaagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 214

DB 362 TGAAGCTGAAGAAAGATATCTCTGAGAGCTGAAGCTGATGATTTCTGTAATCAGAAC 421

OY 215 tctgtcctcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 274

DB 422 TTTCTCTCTCTCTGAGGCTGACAGAGACCTCAAGTGTGCTGCTGCGGAGAGCT 481

OY 275 tgggtcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 334

DB 482 TCGTACAGAGTTATGAGAGAAAGGCTCTCTGAGGCTCTCTCAACCCAGATGCCCT 541

OY 335 ggcctcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 394

DB 542 GGCCTGCGACCTCTCTCTGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 601

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Oy	455	caagagctgcacgttcaagctgagatcttgacctgtccatcttcaagagagctcgaagt	514
Db	662	CAGAGCTCCACGGCAAGCTACGACAAATTTTGGCCCTGTCCACGTTTTCAGCGAGGGTCCAA	721
Oy	515	caagagcaagaggtccgg-----gagacaaaggggacacccctgggtactctggcccc	563
Db	722	CAGGCTTCAGGATTCAGATTCAGATTCAGAGGACCTCTGGGGCCACCTACGCTACTTGGAGCC	781
Oy	564	agaaactgtttgtttaagctaaacggaagagctctcaagacgaatgaactctaaagcttgg	623
Db	782	AGAGCTTTATTGTGATGT-CACTGTGAAGGCTCTTAAAGGATGATGTCTACAGCTTGG	840
Oy	624	gattcctaagtgtggagagaggtctgtcttgaaagaagaagtgttgatgtgcacaacgaacatcaact	683
Db	841	GATCTCTGTGTGGCCAGCTGCTGCTGGCTGGCACAAGAAAGTGTGATGTGACAAAGACTTCACT	900
Oy	684	cgtgtacgaagcagtgctgcacaacagagcgaacagcgctctcatctgagctgagctgccccaaagc	743
Db	901	AATTCGGGAAACAGTGTGTGTGACAGGAGAGTCTCTTCACATGACAGGCTGCTCTCA---	957
Oy	744	cgaggcttcgaagctcccgctctttagaagaacgcgaagagggacgaatgcagctctgcgcggagcag	803
Db	958	--GTACCTGTGAACCCCGCTTGA---AATGTGAAGTTAATGATTCATTTGCGG--GTTTC	1012
Oy	804	tgaagcccaagagcaagacccctctccacagagatgcacacaaaaactatgaattctcca	863
Db	1013	CAGATCCGAAAACAGGCACTTCCTTCCAGAGCTCGAGACCGAGAACCAAAAACCAATGAATTACAA	1072
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Oy	924	caagagacagaaatctgagatcttctatacccaagtgtaagccaaagggagagcaaaatgta	983
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Oy	984	tgcgctttagagagaaacatagaaaaacagcaactctgttaatgtagtcatggtttctgagt	1043
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Oy	1104	taccaagagagagcagggagcaagaagggagcaggtgtccaaagaacctgagcaagagcaatc	1165
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Oy	1164	ttaagattcgaatggtgcccaactctcccagacttccagagacctaaacttttcagaaccagat	1228
Db	1331	TTCTGACACCCGTAAGCTGTGACACTCTTCAGATTTCCACATATTTCCTTCAGAGGCAACAC	1380
Oy	1224	ggccagagccttaacctcaactctgaaacacaaagaatctcttgaaaccccgagagaaatacaggggtctga	1283
Db	1391	ACCTGGGCCCAAGTCTTACTGTGAGACTCTCCGGTCTCTCAACCCCAAAAGGATATGAGGAATGG	1450
Oy	1284	gagagcaagagcagaactctgtccctgcagagcccgccggagccaaatccagctaaagaggagac	1343
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Oy	1344	ggcgtttaaacaatacaactctgtctggagaggtggagagttgaaagaagaacaactatgactat	1403
Db	1508	GGGCTCTGCTTTCACAACTCTTGTGAAGTGAAGATTTGGAACTACAACTCTCTGTGTAGC	1567
Oy	1404	gcacacagacaactgc-----ctgtgccacaatgggagctcttgacactctcgagcaag	1454
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RESULT	7	643 bp	mRNA	linear	EST 06-OCT-2000
LOCUS	BF001916/c				
DEFINITION					
ACCESSION	BF001916				
VERSION	BF001916.1	GI:10702191			
KEYWORDS	EST.				
ORGANISM	human.				
REFERENCE					
AUTHORS					
TITLE					
JOURNAL					
COMMENT					
FEATURES					
source					
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Best Local Similarity	82.8%	Fred: No. 1.5e-106:			
Matches 581: Conservative	0:	Mis. No. 35:	Indels	86:	Gaps 1:
Db	1628	TAGGGCTGGCAGC-CCTTCCAAAGTAGACTTACGACATCATCTGCAAGAGCTGAAGT	1686		
Qy	3515	ctg 1517			
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Db	643	GTCTTCAGAGAGGTGCGAGACTATATCAATCTCGGGGTCTACACGGTAAAGATTCCTG	584		
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Db	643	GTCTTCAGAGAGGTGCGAGACTATATCAATCTCGGGGTCTACACGGTAAAGATTCCTG	584		
Qy	916	tctcagcccaagagcagcaatagagatcttctctccagagctcagcagagagagga 975			
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Qy	976	gaatgatggtctttagggagaaacatagaaacacagcactctcgtaatgatgctatgctt 1035			

Db 523 GATATGATGCTCTAGAGATCCATAGTTAACAGACACTCTGTAATGATGTCATGCTT 464
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 Db 463 TCTGATGCTGTTAAACATCTGACATCTAGAGAGAGCTCCCACTGCTGTTCCATAATATGC 404
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 Db 403 CCGAGCTTACCAAG 344
 1136 ggcacatcttcagatctgagtgcacacactcccaagactccagagagacttaacttcaga 1215
 Db 343 GGCACATCTTACATGATGAGGCCCAACTCCCACTGAGACTCC----- 301
 1216 aaccagatgcccagccttacccttaacttgaagacacaaagtccttgagcccgaggaaatcg 1275
 Db 302 ----- 301
 1276 gggagctgagagagagagagatgaactgctcctgagagaccgagagcgaatccaagtaca 1335
 Db 302 -----AGAGACAG 250
 1336 gggcagcctcgttcaacatatacaactgctcggggtgagagagagagagagagagagag 1395
 Db 249 GGGGACCGCTGCTTAACATATACACTGCTCTGGGGTGCAGATTGAGAGACAACTAC 190
 1306 ttgactaag 1455
 Db 189 TTGACTATGCAACAGACACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 130
 1456 agggagcttgcag 1515
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 1516 tggagcagagcag 1557
 Db 69 TGGAGCAGAGCAG 28
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 LOCUS DKEZP31300939.1 313 (synonym: h1cc2) Homo sapiens cDNA clone
 DEFINITION DKEZP31300939 5', mRNA sequence.
 AL601137
 ACCESSION AL601137.1 GI:15164643
 VERSION EST.
 KEYWORDS human.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 Duesterhoeft, A., Lauber, J., Kewes, H. W., Gassenhuber, J. and Wiemann
 'S.
 EST (Duesterhoeft, et al.)
 Unpublished (1999)
 CONTACT: Duesterhoeft A
 MIPs
 AM R10Pferpitz 18a D-82152 Martinsried, Germany
 This is the 5' sequence of the clone insert
 clone from S. Wiemann. Molecular Genome Analysis, German Cancer
 Research Center (DKFZ), Email: s.wiemann@dkfz-heidelberg.de;
 sequenced by Qiagen (Hilden/Germany) within the cDNA sequencing
 consortium of the German Genome Project.
 No 31 sequence available.
 This clone (DKFZP31300939) is available at the RZPD in Berlin.
 Please contact the RZPD: Ressourcenzentrum, Heubenerweg 6, 14059
 Berlin-Charlottenburg, GERMANY; Email: clone@rzd.de.
 location/Qualifiers
 1. 758
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 Db 252 CTGAG 311
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 Db 312 AGGAAGTGAGGCTAGATGAG 371
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 Db 372 GTCAAGAGCAG 431
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 Db 492 TCCCTGTGAG 551
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 Db 552 CTGAAGAAG 611
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 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 NIH-MGC
 TITLE NIH-MGC
 AUTHORS NIH-MGC
 JOURNAL NIH-MGC
 COMMENT NIH-MGC
 Contact: Robert Strausberg, Ph.D.
 Email: rgs@nihs.nih.gov
 Tissue Procurement: Life Technologies, Inc.
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LAM1572 row: a column: 20
 High quality sequence stop: 616.

FEATURES

Source

FEATURES	SOURCE	Location/Qualifiers
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		/clone_id="NH_MCC_120"
		/lab_host="DH10B"
		/lab="Organ: pooled pancreas and spleen; Vector: pCVC-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA source anonymous pool of spleen and pancreas from 28 yo male. Library is oligo-dT primed and directionally cloned (EcoRV) site is destroyed upon cloning). Average insert size 1.5 kb. Insert size range 1-2.5 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 023. Note: this is a NIH_MCC Library."
BASE COUNT		134 a
ORIGIN		188 c 177 g 117 t

**BASE COUNT
ORIGIN**

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Best Local Similarity	99.1%;	Pred. No. 1.1e-102;		
Matches 451; Conservative	0;	Mismatches 4;	Indels 0;	Gaps 0;

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Db	162	atgtcgtgtccgtcaagttatgacccacacgcgtgtgcacccctcgtgtctccatccagagaa	221
OY	61	ctcgagaaaccaaagacgtcgtctcgagcaaaagacggtgttcgagcaagtggttcgcggtcacaat	120
Db	222	ctcgagaaaccaaagacgtcgtcgcgcacaaagccgggttccgcacagttcttcgcgcgcacaaat	281
OY	121	aggaagatggtgggtgtcaggtgtgtgtggtgtcgaagatcgttaaaatctggaaagtgatataccaaagag	180
Db	282	aggaagatggtgggtgtcaggtgtgtgtggtgtcgaagatcgttaaaatctggaaagtgatataccaaagag	341
OY	181	gtcaaaagccatctggtcaaaagtcctgtgaataacgaatcctgtgttcgcctcagaagaaggtttatctag	240
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Db	402	aaggtgtgaatctggtgacccaagaatccccaagccggtctctgtgtgaactaaatccatgtgaaagacgac	461
OY	301	tcacctgtccgggtgtcgtcgtcagtcaccagtgcacctctggccctctggccgctccctcttgcgcgcgt	360
Db	462	tcacctgtccgggtgtcgtcgtcagtcaccagtgcacctctggccctctggccgctccctcttgcgcgcgt	521
OY	361	ctgaaagaagctgtgtccttggatgttttaacctctgcagacccaagaaccccggtgtcctctctgcac	420
Db	522	ctgaaagaagctgtgtccttggatgttttaacctctgcagacccaagaaccccggtgtcctctctgcac	581
OY	421	cggtgacctcaagaacatcccaagctctgcgcgggtccc	455
Db	582	cggtgacctcaagaacatcccaagctctgcgcgggtccc	616

RESULT 10
AA227673
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE

LOCUS	440 bp	MRNA	linear	EST 06-AUG-1997
DEFINITION	z555009.f1 Soares.NHMP.L51	homo sapiens	CDNA	IMAGE:667313
ACCESSION	AA227673			
VERSION	AA227673.1	GI:1849253		
KEYWORDS	5', mRNA sequence.			
SOURCE	human.			
ORGANISM	Homo sapiens			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
AUTHORS	1 (bases 1 to 440) Hillier, L., Allen, M., Bowles, L., Dubuque, T., Getse, G., Jost, S., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Thelings, B., White, Y., Wyllie,			

TITLE
JOURNAL
COMMENT

TITLE 'T', Waterston, R. and Milson, R.
JOURNAL Mashu-Merck EST Project 1997
COMMENT Unpublished (1997)
Contact: Milson Rk
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@waterston.wustl.edu
This clone is available royalty-free through INL; contact the
IMAGE Consortium (info@image.lnh.gov) for further information.
Insert Length: 829 Sd Error: 0.00
Seq primer: -26m3 rev2 ET from Amer sham.

FEATURES

BASE COUNT
ORIGIN

131 a 119 c 111 g 79 t

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pregnant uterus"
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(Pharmacia) with a modified polylinker; site.1: Not I;
site.2: Eco RI. Equal amounts of plasmid DNA from three
normalized libraries (melanocyte 2NbMv pregnant uterus
NBMPU) and fetal heart NBH19N) were mixed and as circles
was used as tracer in a subtractive hybridization, this DNA
reaction. The driver was PCR-amplified cDNAs from pools of
5,000 clones made from the same 3 libraries. The pools
consisted of 1.M.A.G.E. clones 260232-265223,
340488-345479, and 484488-489479.
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BASE COUNT
ORIGIN

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Qy	999	catagaaacacagacactctcgttaatgcatgcatggtcttcgtatggtctcgtatggctaaacaactctga	1058
Db	61	catgaaacacacacacactctcgttaatgcatgcatggtcttcgtatggtctcgtatggctaaacaactctga	120
Qy	1059	tctagagagagctcccaagctctgttctcctaaataatgcccgagcttaccagaagagagccag	1118
Db	121	ttctagagagagctcccaagctctgttctcctaaataatgcccgagcttaccagaagagagccag	180
Qy	1119	ggccaagaagagagctcaggtcttcacaagaacctctggaacagagacactcttcagatctcgatggc	1178
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Qy	1179	ccaacactctcccaagacttcagaagacacttcaacttcagaaacacagatggccagccctacttc	1238
Db	240	ccaacactctcccaagacttcagaagacacttcaacttcagaaacacagatggccagccctacttc	299
Qy	1239	aactcgaaacccaagtctctggaaccccgagggatctcagggggtctggagagcaagcattgaa	1298
Db	300	aactcgaaacccaagtctctggaaccccgagggatctcagggggtctggagagcaagcattgaa	359
Qy	1299	ctgttctctgagaagaccccgagagcaaatctcaatcaagagagggcgaacgcgtctcgttcaactata	1358
Db	360	ctgttctctgagaagaccccgagagcaaatctcaatcaagagagggcgaacgcgtctcgttcaactata	419
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Db	420	caactgctctgggtgtgaagt 440	

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ACCESSION BF359285
VERSION BF359285.1 GI:11318461
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 432)
AUTHORS Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Brites,M.R.,
Nagai,M.A., da Silva,N.J., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,
M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.G.
TITLE Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE 20202663
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-3704927
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the PAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?l1=RC6&l2=RC6-ET0081-
100700-012-B10&l3=2000-07-10&l4=1)
Seq primer: puc 18 forward
High quality sequence start: 36
Location/Qualifiers
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1..432
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="ET0081"
/dev_stage="Adult"
/note="Organ: Lung_tumor; Vector: puc18; Site:1: Smal;
Site:2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
Profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
BASE COUNT 88 a 143 c 109 g 90 t 2 others
ORIGIN
Query Match 25.3%; Score 393.8; DB 10; Length 432;
Best Local Similarity 96.6%; Pred. No. 6.7e-89;
Matches 401; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

DB 243 GTCAGGCCATGCGCACTGATGAACGATTCGTGCGCCCTAGAGAGGGTTATCGAG 184
OY 241 aaggtgaactgagaccagaatcccaagccgctcgtgtaactaattcatggaacgcgc 300
DB 183 AGGTGAACCTGGACACAAAGATCCCAAGCGGCTGTGTGACTTAATTCATGAGAACGGC 124
OY 301 tccctgtcggggcgtcgtcagctccagctccctgtgcccctggccctcttcgcgcga 360
DB 123 TCCCTGTGCGGCCCTGTGCAAGTCAGTCAGTCCCTGCGCCCTGCGCTCTTGTGCGCCTG 64
OY 361 ctgaagaagtggtgcttggtgatttaccctgcagcagccagccgcgtgctcc 415
DB 63 CTCGAAGAACGTGCTGTGGAGATGTTACTGACACGACATATCTAGGGGCTCC 9
RESULT 12
LOCUS B1905455 906 bp mRNA linear EST 16-OCT-2001
DEFINITION 60316794/F1 NC1_CGAP_Lu33 Mus musculus cDNA IMAGE:5256010 5',
B1905455 mRNA sequence.
ACCESSION B1905455
VERSION B1905455.1 GI:16167978
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Scuriognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 906)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/
TITLE NIH-MGC National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabs-remail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.
cDNA library arrayed by: The I.M.A.G.E. Consortium (LULN)
DNA Sequencing by: InCyte Genomics, Inc.
Clone distribution: NC1-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LULN at:
http://image.llnl.gov
Plate: LULN1646 row: n column: 11
High quality sequence start: 28
Location/Qualifiers
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source
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/organism="Mus musculus"
/strain="C57BL/6J"
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/clone_image="5256010"
/clone_lib="NC1_CGAP_Lu33"
/tissue_type="Pooled Lung tumors"
/lab_host="DH10B (phage-resistant)"
/note="Organ: Lung; Vector: p773b-Pec (Pharmacia) with a
modified polylinker; Site:1: NotI; Site:2: EcoRI; 1st
strand cDNA was prepared from mRNA obtained from pooled
lung tumors with a Not I - oligo(dT) primer [5']
TGTACCAATCTCAAGTCGAGCGCGCCGCTCTTTTCTTTTCTTTT 3'].
Double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not
I and Eco RI sites of the modified p773 vector. Library
went through one round of normalization, and was
constructed by Bento Soares and M. Fatima Bonaldo."
BASE COUNT 188 a 245 c 208 t
ORIGIN
Query Match 24.9%; Score 388.4; DB 10; Length 906;
Best Local Similarity 74.7%; Pred. No. 2.2e-87;
Matches 560; Conservative 0; Mismatches 171; Indels 19; Gaps 5;
OY 1 atgtcgtgcacagattatgcccagcgtgccccgc-----cccttggtgttcacacgag 57

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Db 136 ATGCTCTCTCTCAAGTTAAGGCTTACTGTCGCTACAGGGTCTCTCTGTCGACCGTGAA 195
Oy 58 gaactcggaagaccagaagctcgccgcaagaacgggttcggacagtggttcggcgcaaa 117
Db 196 GAATGAAAGAACTGACG-TTGCTGGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 254
Oy 118 cacaagaagtgaggcgaagctgagcagcgaagcgaagcgaagcgaagcgaagcgaagcgaag 177
Db 255 CACAGAAACATGAAACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 314
Oy 178 gaagtcgaagcctgagcagcctgagcagcctgagcagcctgagcagcctgagcagcctgag 237
Db 315 GAGGTGAAGCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 374
Oy 238 gaagaagtgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 297
Db 375 GAGGACCTCAAGTGGAGATTCGTCGCGGAGAGCTGTCGTCGTCGTCGTCGTCGTCGTCGTC 434
Oy 298 ggtccctcgtcgggagctgctgctgctgctgctgctgctgctgctgctgctgctgctgctg 357
Db 435 GGTCTCTCTCCAGGCTGCTCTCTCAACCCAGTCCCTGCGCTGCGCTCTCTCTCTCTCTCT 494
Oy 358 ctgctgaagaagtggtgctgctgagtgctgctgctgctgctgctgctgctgctgctgctg 417
Db 495 CTGCTGAGGAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 554
Oy 418 cagcaggaagcctcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 477
Db 555 CACCGGAGACTCAAGCCCTTAACATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 614
Oy 478 gatttggtcgtcgaatctcagaagtgctcagaagtgctcagaagtgctcagaagtgctcaga 530
Db 615 GATTGTGGCTGTCTCAAGTTCAGGAGAGGTCCTCAGTTCAGGAGAGGTCCTCAGTTCAGGAG 674
Oy 531 ----gagaccaggggagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 586
Db 675 TCCAGGAGCTGTGCGGCGCACCCCTAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 734
Oy 587 ggaagagcctcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 645
Db 735 TGAAGGCTTTAAAGGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 794
Oy 646 gctggaagagagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtgag 702
Db 795 GCTGGCGAGAAAGCTAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 854
Oy 703 aacagcagagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 732
Db 855 ACCGCGAGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 884

RESULT 13
LOCUS BF359287 414 bp mRNA linear EST 22-NOV-2000
DEFINITION RC6-ET0081-100700-012-C04 ET0081 Homo sapiens cDNA, mRNA sequence.
ACCESSION BF359287
VERSION BF359287.1 GI:11318463
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 414)
Dlaa Neto E., Garcia Correa R., Verjovski-Almeida S., Britones M.R.,
Nagal M.A., de Silva W. Jr., Zago M.A., Bordin S., Costa F.F.,
Goldman G.H., Carvalho A.F., Matukuma A., Balde G.S., Simpson D.H.,
Brunstein A., deoliveira P.B., Bucher P., Jongeneel C.V., O'Hare
M.J., Soares F., Brentani R.R., Reis L.F., de Souza S.J. and
Simpson A.J.
TITLE Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

```

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MEDLINE 20202663
CONTACT: Simpson A.J.G.
COMMENT Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
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Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL:
(http://www.ludwig.org.br/scripts/gethtml2.pl?rl=RC6et2-RC6-ET0081-
100700-012-C04et3-2000-07-10et4-1)
Seq primer: puc 18 forward
High quality sequence start: 23
High quality sequence stop: 374.
Location/Qualifiers
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="ET0081"
/dev_stage="Adult"
/note="Organ: Lung-tumor; Vector: puc18; Site1: SmaI;
Site2: SmaI; A mini-library was made by cloning products
derived from ORFESTS PCR (U.S. Letters Patent Application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
BASE COUNT 86 a 137 c 105 g 86 t
ORIGIN

Query Match 24.5% Score 382; DB 10; Length 414;
Best Local Similarly 98.7% Pred. No. 6.3e-86;
Matches 385; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Oy 1 atgtcgtcgtcgaatgtagccagcagcgtgcccgcgcctctggtgctcagcagaa 60
Db 411 ATGTGTCGTCGAAGTTAAGGCGCAAGCCGTCGCCGCCCTGTCGTCGTCGTCGTCGTCGTCG 352
Oy 61 ctggaagaccagagagctgctgagcagaagcaggttgagcagcagtgctcggcgcaaacat 120
Db 351 CTGGAGAACGAGGAGCTGCTGCGCAAGCGGGTTCGGCAAGTGTCCGGCGCAACAT 292
Oy 121 aggaagtgaggctacagtgctgagcagtcagagtcgtaaacctggaagcgatcagaggag 180
Db 291 AGGAAGTGCGGCTACGATGTGCGGCTCAAGATCGTAATCGAAGCGATATCCAGGAG 232
Oy 181 gtcaagagcagtcagagcctgagataacgaatcgtgctgctcagcagagggctacagag 240
Db 231 CTCMAAGCCATGCGAAGTGTGGAATTCGTCGCTGCGCTGAGAGGCTATTCAG 172
Oy 241 aagtggaactgggaacagatgccaaagccgcttggtgcttaattctggagaagcgc 300
Db 171 AAGGTGAACGTGGAGCAAGATCCCAAGCGGCTGTGGTCAATTAATCAAGAAAGCGC 112
Oy 301 tccctcgtgagtgctgagtgagtgccagtgccctcgccctgagcagcctcttgcgcctg 360
Db 111 TCCCTGTCGCGGCTGCTGCAATGCCAGTGCCCTGCGCCCTGCGCCCTCTTGTCCGCGCTG 52
Oy 361 ctgaagaagtggtgctgagtgagtgctgagtgagtgagtgagtgagtgagtgagtgag 390
Db 51 CTGMAAGAGAGTGTGCTGGAATGTTTCC 22

RESULT 14
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DEFINITION RC6-ET0081-130700-011-H04 ET0081 Homo sapiens cDNA, mRNA sequence.
ACCESSION BF359303
VERSION BF359303.1 GI:11318479
KEYWORDS EST.

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SOURCE human.
ORGANISM Homo sapiens
REFERENCE Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
AUTHORS Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., de Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bal, G.S., Simpson, D.H., Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.
TITLE Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE 20202663
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Rui Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?rl=RC6a2-RC6-ET0081-130700-011-H04613-2000-07-13&rl=1)
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High quality sequence start: 16
High quality sequence stop: 206.
Location/Qualifiers
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/organism="Homo sapiens"
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/clone_lib="ET0081"
/dev_stage="Adult"
/note="Organ: Lung; tumor; Vector: puc18; Site:1: Smal; Site:2: Smal; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the puc 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
BASE COUNT 96 a 117 c 139 g 98 t 1 others
ORIGIN
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Best Local Similarity 95.8%; Pred. No. 1.7e-85;
Matches 390; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

DB 337 TGTCTGGCTGCTGACATCCAGTCCCTGCGCCCTGCTCTTGTCCGCTCTCTCA 396
OY 365 aagaagtgctgcttggaatcttactctgacagaccagaccggtg 411
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DB 397 AAGAAGTGTGCTTGATGTTACTGACAGACATATACCTAGNG 443
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DEFINITION RC6-ET0081-070800-013-B12 ET0081 Homo sapiens cDNA, mRNA sequence.
ACCESSION BF359467
VERSION BF359467.1 GI:11318448
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
AUTHORS Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., de Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bal, G.S., Simpson, D.H., Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.
TITLE Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE 20202663
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Rui Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?rl=RC6a2-RC6-ET0081-070800-013-B12&rl=2000-08-07&rl=1)
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High quality sequence start: 27
High quality sequence stop: 315.
Location/Qualifiers
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/db_xref="taxon:9606"
/clone_lib="ET0081"
/dev_stage="Adult"
/note="Organ: Lung; tumor; Vector: puc18; Site:1: Smal; Site:2: Smal; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the puc 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
BASE COUNT 79 a 126 c 102 g 81 t
ORIGIN
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Best Local Similarity 96.3%; Pred. No. 2.8e-80;
Matches 368; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

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OY 150 gatcgfaaaactgaaaggagatatccaggaggctcaggccatgccaagtctgatataga 209
Db 268 GATCGTAAACTCGAAGCCGATATCCAGGAGAGCTTAGGCCATGGCAGTGTGATMACGA 209
OY 210 atctgtgttcgagcctagaagggttatcgagaaggtgaactgagaccagaatcccaagcc 269
Db 208 ATTCGTGCTGCGCCTAGAAAGGGGTTATCGAGAGGTGACTGGGACCAAGATCCCAAGCC 149
OY 270 ggcctcgtgactaaatcatgagaaagagcgtccctgtcgggggtgtgtgcaatgcccaatg 329
Db 148 GCGTCTGCTGACATAATTGATGAGAAACGGCTCCTTGTCAAGGCTCTGCACTCCACATG 89
OY 330 cccctggccctggcgcgtcccttgcgcgtctgaagaagtggtgcttgagatgtttaa 389
Db 88 CCTTCGGCCCTGCGCCTCTTTCCTTGGCCGCTGTGAAGAAGTGCTGCTTGGATGTTTAA 29
OY 390 cctgcagagacagaaaccggtg 411
Db 28 CCGCACGACATATACCTTAGGG 7
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Search completed: August 13, 2002, 20:36:21
Job time: 2169 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 13, 2002, 20:04:37 ; Search time 2051.96 Seconds
(Without Alignment)
15878.778 Million cell updates/sec

Title: US-09-762-491-5

Perfect score: 1557
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1797656 segs, 10463268293 residues

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

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1: gb-da: *
2: gb-hlg: *
3: gb-in: *
4: gb-om: *
5: gb-ov: *
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7: gb-ph: *
8: gb-pl: *
9: gb-pr: *
10: gb-ro: *
11: gb-sts: *
12: gb-sy: *
13: gb-un: *
14: gb-vi: *
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16: em-fun: *
17: em-hum: *
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23: em-pat: *
24: em-ph: *
25: em-pl: *
26: em-ro: *
27: em-sts: *
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29: em-vi: *
30: em-hlg-hum: *
31: em-hlg-inv: *
32: em-hlg-other: *
33: em-hgo-inv: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	1557	100.0	1557	9	AF156884	AF156884 Homo sapi
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4	1536.4	98.0	1873	6	AR105327	AR105327 Sequence
5	1526.4	98.0	1873	6	AX067676	AX067676 Sequence
6	673.6	43.3	1437	6	AX100029	AX100029 Sequence
7	672.2	42.0	2015	10	AF036537	AF036537 Rattus no
8	654.2	42.0	1833	10	AF178953	AF178953 Mus muscu
9	377.6	24.3	196533	9	CNS007V1	AL036810 Human chr
10	379.6	21.2	1073	6	AX056439	AX056439 Sequence
11	193.6	12.4	240105	6	AC098877	AC098877 Mus muscu
12	135.8	8.7	254	6	AX211236	AX211236 Sequence
13	109	7.0	3876	9	AR027424	AR027424 Homo sapi
14	107.4	6.9	3879	9	HS0478016	AJ278016 Homo sapi
15	107.4	6.9	3882	9	AB047783	AB047783 Homo sapi
16	104	6.7	2499	6	AX166548	AX166548 Sequence
17	95.2	6.1	3559	10	AF302127	AF302127 Mus muscu
18	88.4	5.7	2348	6	AX207411	AX207411 Sequence
19	74	4.8	124516	9	AP001615	AP001615 Homo sapi
20	74	4.8	219256	9	AP001743	AP001743 Homo sapi
21	73.2	4.7	139651	2	OSJN00183	AL662984 Oryza sat
22	71.8	4.6	144720	8	AC087544	AC087544 Oryza sat
23	71.8	4.6	193068	8	AP003455	AP003455 Oryza sat
24	68.4	4.4	3897	1	NCU40656	U40656 Myxococcus
25	63.4	4.1	2537	3	ACU67055	U67055 Acanthamoeb
26	63.2	4.1	177034	9	AP002840	AP002840 Homo sapi
27	62.8	4.0	152859	2	AC096518	AC096518 Rattus no
28	62.8	4.0	120538	2	AP004082	AP004082 Oryza sat
29	61.8	4.0	175406	2	AC087128	AC087128 Mus muscu
30	60.6	3.9	151289	2	AP003228	AP003228 Oryza sat
31	58	3.7	3018	6	AX119982	AX119982 Sequence
32	58	3.7	4417	9	AB040892	AB040892 Homo sapi
33	58	3.7	4417	9	AB040892	AB040892 Homo sapi
34	57.8	3.7	999	6	A98935	A98935 Sequence 2
35	57.8	3.7	1203	6	A98939	A98939 Sequence 6
36	57.8	3.7	1260	9	AF014401	AF014401 Homo sapi
37	57.8	3.7	1392	9	AF006689	AF006689 Homo sapi
38	57.8	3.7	1425	9	AF022805	AF022805 Homo sapi
39	57.8	3.7	121615	2	AP003981	AP003981 Oryza sat
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41	56.8	3.6	146670	8	AP003250	AP003250 Oryza sat
42	56.6	3.6	143587	2	AC093018	AC093018 Oryza sat
43	56.4	3.6	106719	2	AP003818	AP003818 Oryza sat
44	56.4	3.6	131531	2	AP003813	AP003813 Oryza sat
45	56.2	3.6	1461	9	AF013588	AF013588 Homo sapi

ALIGNMENTS

RESULT 1
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LOCUS AF156884
DEFINITION Homo sapiens RIP-like kinase (RIP3) mRNA, complete cds.
ACCESSION AF156884
VERSION AF156884.1 GI:5059424
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 1557)
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
AUTHORS Yu, P.W., Huang, B.C., Shen, M., Quast, J., Chan, E., Xu, X., Nolan, G.P.,
Payan, D.G. and Luo, Y.
IDENTIFICATION OF RIP3, A RIP-LIKE KINASE THAT ACTIVATES APOPTOSIS
AND NF-KAPPA-B
CURR. BIOL. 9 (10), 539-542 (1999)

TITLE JOURNAL MEDLINE
99272740
2 (bases 1 to 1557)
REFERENCE
AUTHORS Yu, P.W., Huang, B.C., Shen, M., Quast, J., Chan, E., Xu, X., Nolan, G.P.,
Payan, D.G. and Luo, Y.
DIRECT SUBMISSION
SUBMITTED (04-JUN-1999) Rigel, Inc. 240E Grand Ave., San Francisco,

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DB	61	CTGGAGAACCAAGACGTCGTGCGCAAGACGGTTCGCAAGTGTCCGGCGCAACAT	120		
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DB	121	AGGAATGGGGCTACGAATGTGCGGTCAAGTCTAATCTCGAAGCGATATCCAGGAG	180		
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DB	301	TCCCTGTGAGGCTCTGCAATGCCAGTGCCTGCGCCTGCGCTCTTGGCCGCTG	360		
QY	361	ctgaagaagaatggtgctctggaatcttaccctgcagcaacgaagaccggctgctctgac	420		
DB	361	CTGAAGAAGAATGCTCTGGATTTTACCTGCACACAGAACCGGCTGCTCTGAC	420		
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QY	481	tttgacctgtccaaatttcagggaagctcacagtccaggacaggtccgggagccaggg	540		
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DB	601	GCCAGTGACGTCTACAGCTTCGGGATCCTTAATGCGGAGTGTCTCTCGAAGAGAAATT	660		
QY	661	gaattgcaaacgaaacacactactctgtgaagcaagtgtgcaaacaggcaaacggcct	720		
DB	661	GAGTTGCCAACCCAAACACACTCTGTACCAACACTGTGCAACGGCAGAACGGCCT	720		
QY	721	tcaattgctgagctgcccgaagccggctggaactcccggtctgaagaagactgaagaag	780		
DB	721	TCATTGGCTGAGCTGCCCAAGCCGGCTGAGACTCCGGCTTAAGAGACTGAAGAGAG	780		
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QY	901	gtaagaatctctgctgctgagctcaagaagcgcaatagaagatctctcaccagaagta	960		
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QY	1021	aatgattcaatgcttctgagtgagctaaacaaactgaatcagaagagcctccagctct	1080		
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DB	1081	GTTCTTAAAAATGCCCGGCTTACCAAGAGAGCGACAGCAAGAGCAAGTTCCTCA	1140		
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ACCESSION	ARI05328				
VERSION	ARI05328.1 GI:12818925				
KEYWORDS					
SOURCE	Unknown.				
ORGANISM	Unknown.				
	Unclassified.				

REFERENCE 1 (bases 1 to 1557)

AUTHORS Gomes, B. Charles., Kasof, G. M. and Prosser, J. Caroline.

TITLE Protein activator of apoptosis

JOURNAL Patent: US 6096539-A 2 01-AUG-2000;

FEATURES Location/Qualifiers

SOURCE

1..1557

BASE COUNT 395 a 422 c 448 g 291 t 1 others

ORIGIN

Query Match 99.5%; Score 1548.6; DB 6; Length 1557;

Best Local Similarity 99.6%; Pred. No. 0;

Matches 1551; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

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Sequence 2 from Patent WO0077200.

AX067677

AX067677.1 GI:12329571

KEYWORDS

SOURCE human.

ORGANISM Homo sapiens

Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 1557)

AUTHORS Gomes, B. C., Kasof, G. M. and Prosser, J. C.

TITLE Receptor interacting protein rip3

JOURNAL Patent: WO 0077200-A 2 21-DEC-2000;

Astrazeneca AB (SE)

Location/Qualifiers

FEATURES

SOURCE

1..1557

BASE COUNT 395 a 422 c 448 g 291 t 1 others

ORIGIN

Query Match 99.5%; Score 1548.6; DB 6; Length 1557;
 Best Local Similarity 99.6%; Pred. No. 0;

Matches 1551; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

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LOCUS AR105327
DEFINITION Sequence 1 from patent US 6096539.
ACCESSION AR105327
VERSION AR105327.1 GI:12818924
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1873)
AUTHORS Gomes, B. Charles., Rasof, G. M. and Prosser, J. Caroline.
TITLE Protein activator of apoptosis
JOURNAL Patent: US 6096539-A 1 01-AUG-2000;
FEATURES
source 1..1873
BASE COUNT 471 a 531 c 518 g 353 t
ORIGIN

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Query Match 98.0%, Score 1526.4; DB 6; Length 1873;
Best Local Similarity 99.1%, Pred. No. 0;
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Db 61 CTGGAAACACAGAGAGCTGCTCGCAAGCGGTTCGCGACAGTGTCCCGCGCCAACT 120
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 Db 405 AAGCTCGCGCGCTCGAGCCAAATCCCAAGCCGGCTCGGTGATTAATCATAGGAAC 464
 Qy 298 ggcctcctgtcggggctcgtcgtcagtcgccagtcgcccctgcccgtccttgcagc 357
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 LOCUS AK067676 Sequence 1 from Patent WO007720.
 DEFINITION AK067676
 ACCESSION AK067676
 VERSION AK067676.1 GI:12329570
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 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 1873)
 AUTHORS Games, B.C., Kasof, G.M. and Prosser, J.C.
 TITLE Receptor interacting protein rip1
 JOURNAL Patent: WO 0077200-A 1 21-Dec-2000;
 Astrazeneca AB (SE)
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DEFINITION	Sequence 1 from Patent WO0119990.				
ACCESSION	AX100029				
VERSION	AX100029.1	GI:13539035			
KEYWORDS					
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REFERENCE	1 (bases 1 to 1437)				
AUTHORS	Virca,G.D. and Bird,T.A.				
TITLE	RIP-3-like death-associated kinase				
JOURNAL	Patent: WO 0119990-A 1 22-MAR-2001; IMMUNEX CORPORATION (US)				
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REFERENCE	AUTHORS	TITLE
JOURNAL	Chen, K.H. and Tang, J.	A hemocysteine-responsive gene cloned from WKY VSMCs by differential display
REFERENCE	2 (bases 1 to 2015)	Unpublished
AUTHORS	Chen, K.H. and Tang, J.	
JOURNAL	Submitted (03-DEC-1997)	Institute of Cardiovascular Research, Beijing Medical University, Xueyuan Rd. 38, Beijing 100083, China
REFERENCE	3 (bases 1 to 2015)	
AUTHORS	Chen, K.H. and Tang, J.	
JOURNAL	Submitted (21-MAY-2001)	Institute of Cardiovascular Research, Beijing Medical University, Xueyuan Rd. 38, Beijing 100083, China
REMARK	Sequence update by submitter	
COMMENT	On May 21, 2001 this sequence version replaced gi:4104520.	
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RESULT 8
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DEFINITION Mus musculus receptor interacting protein 3 (Rip3) mRNA, complete
ACCESSION AF178953
VERSION AF178953.1 GI:6063100
KEYWORDS
SOURCE
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  Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Eumetazoa; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
  1. (bases 1 to 1833)
  Pazdernik, N.J., Donner, D.B., Goebel, M.G. and Harrington, M.A.
  Mouse Interacting Protein 3 Does Not Contain a Caspase-Recruiting
  Or a Death Domain but Induces Apoptosis and Activates NF-kappaB
  Mol. Cell. Biol. 19 (1999) In press
  2. (bases 1 to 1833)
  Pazdernik, N.J., Donner, D.B., Goebel, M.G. and Harrington, M.A.
  Direct Submission
  Submitted (19-AUG-1999) Walther Oncology Center, Indiana University
  School of Medicine, 1044 West Walnut Street, Indianapolis, IN
  46202, USA

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D	991	TTCCAGGACTGCGAACCAGAAACCAATGAAGATTTCATCTGTGAAAGGACAAAGTACAT	1050
O	886	gctcgtctccacggtaaagatcttcctgtctcagctcacaagcagcaatagagatt	945
D	1051	GCCTGCTGTCCGAGCTTAACCATTTCTGTCTCGACACAAACATGTGCANAACTTG	1110
O	946	tccatcccaagagtcagggccaaaggggagacagaataatgtgctcttaagaaacatataga	1005
D	1111	TTCTGCCAGAGAGCCAAAGCCAAAGAGGACAGAAATGATTCGCCGAGGAGAAC-----	1163
O	1006	aaccagcactctcgtatagatgtcatgtgttcttgggtgtcttaaaacaaactgaatcaga	1065
D	1164	-----CATGTTTCTAAATAGCTGGACCCCTCTGCATTTGGAG	1200
O	1066	gagctcccaagctctgtctcctaaaaaatgcccgagaccttacaagaagagcagggcacaa	1125
D	1201	GAAACCTCTCGGACCAAGTTCCTCGAATAATGTC-----TGAAGAGCCAAAGCCAG	1268
O	1126	gaaggagcaggttcccaagaacctgtgagacagcagacatcttcaagcttgaatgtgcacact	1185
D	1249	GACACATCTAGTTTGGGCTGTGCCACACAGCAAGAAAGATCTTCTGACCCCGTGTGGACT	1308
O	1186	cccccaaacccaggaagacttaacttcaagaacacagatgtgcacagcccttaactcaactga	1245
D	1309	CTCTCAATTCACAACTTTTACCTTTCAGAGGACACAAACCTGGCCAGTCTTTACTGAC	1366
O	1246	acacaaagctctggaaccccgaggaatcaggggggtgagacaaagacatgaactgtctc	1305

Db	1369	ACTCCGGGCTCTCCACCCCCAAGAAATGAGGAGATGGAAGAGACAGGCACTCCTTGGTAT	1428
Oy	1306	tcgacgagcccccgagccaatccagtaacagggcgacgcgcctcgtttacatatatacaactgac	1365
Db	1429	CCCTGGACCCCC---ACGGAATCCATATGACAGAGGCAACGGGCTCTCCTCTTCACAACTGT	1485
Oy	1366	tctgggggtgcaagttgaggacacacactacttgactctatgcaacagacaaactgc-----	1418
Db	1486	TCGTAACTGCAGATTTCGGAACATCAACTCTCTTGGTTACACACACCAAGAACTACTCGCTCA	1545
Oy	1419	--cttgcaccacatgggggcttggcacctctcgggcaagggaggggcttgcgacccccca	1476
Db	1546	AGTTTCGGCCAAAGTATATACCACACACAGTTTCGGCAGGGGGTATGGGGCTTCGGAGC-CTTTCCA	1604
Oy	1477	ccagtaggttcgcaagaagggccctaaatcctaaagcccg	1517
Db	1605	CAGATMACTTCAGACAAATCACTGCACAAAGCCTCAATGTG	1645

RESULT	9
CNS000YV1	
LOCUS	
DEFINITION	CNS000YV1 196533 bp DNA linear PRI 04-JUL-2001
ACCESSION	
VERSION	
KEYWORDS	Human chromosome 14 DNA sequence BAC R-93489 of library RPCT-11 from chromosome 14 of Homo sapiens (Human), complete sequence.
SOURCE	AL096870.5 GI:14625739
	HTG; HTGS_ACTIVEFIN.
	human.

REFERENCE	1 (bases 1 to 196533)
AUTHORS	Hallig, R., Petit, J.L., Vico, V., Dasilva, C., Robert, C., Wincker, P., Brolier, P., Catrollico, L., Barbe, V., Pelletier, E., Arliguenave, F., Levy, M., Eskenberg, R., Bruls, T., debernardinis, V., Craud, C., Chapuy, G., Saurin, W. and Weissenbach, J.
TITLE	Sequencing of the human chromosome 14
JOURNAL	Unpublished
REFERENCE	2 (bases 1 to 196533)
AUTHORS	Genoscope.
TITLE	Direct Submission
JOURNAL	Submitted (04-JUL-2001) Genoscope - Centre National de Sequencage :

COMMENT

Center: Genoscope / Centre National de Séquençage
Center code: GS
Web site: <http://www.genoscope.cns.fr/>
Contact: SeqRef@genoscope.cns.fr

```

The following BAC sequence is oriented from the T7 to the sp6 end.
Upstream BAC (overlapping the T7 end) : R-80A15 (AC-AL13880)
Downstream BAC (overlapping the sp6 end) : R-468E2 -----
Summary Statistics
Assembly program: Phrap; version 2.0
Quality coverage: 9.97x in Q20 bases; 8um-of-coverage

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-----Overall quality chart :-----
Range      :      bases
0           :
1 - 9      :
10 - 19    :
20 - 29    :      16
30 - 39    :      48
40 - 49    :      1545
50 - 59    :      6383
60 - 69    :      10296
70 - 79    :      25537
80 - 89    :      61534
90 - 99    :      91204
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FEATURES source	Percentage of bases with a quality value >= 40 : 99 %.	Location/Qualifiers
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STS	11917. .12046	/note="matching EMBL:R11213 Rdb:RH53655 dbSTS:STS29995 Identified using the e-PCR software (G. Schuler)"
STS	53793. .53918	/note="matching EMBL:AA227560 Rdb:RH91896 dbSTS:STS64900 Identified using the e-PCR software (G. Schuler)"
STS	71412. .71564	/note="matching EMBL:AA044828 Rdb:RH93999 dbSTS:STS66992 Identified using the e-PCR software (G. Schuler)"
STS	73064. .73203	/note="matching EMBL:G14793 Rdb:RH8035 dbSTS:STS15133 Identified using the e-PCR software (G. Schuler)"
STS	76074. .76306	/note="matching EMBL:AA021034 Rdb:RH75381 dbSTS:STS52469 Identified using the e-PCR software (G. Schuler)"
STS	80953. .81105	/note="matching EMBL:AA258432 Rdb:RH94061 dbSTS:STS67054 Identified using the e-PCR software (G. Schuler)"
STS	81788. .82011	/note="matching EMBL:AA009760 Rdb:RH75263 dbSTS:STS52351 Identified using the e-PCR software (G. Schuler)"
STS	81795. .81885	/note="matching EMBL:Z41293 Rdb:RH36692 Rdb:RH36650 dbSTS:STS32281 Identified using the e-PCR software (G. Schuler)"
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STS	99021. .99159	/note="matching EMBL:H22572 Rdb:RH78575 dbSTS:STS55316 Identified using the e-PCR software (G. Schuler)"
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STS	dbSTS:STS27395	Identified using the e-PCR software (G. Schuler)"
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STS	126995. .127359	/note="matching EMBL:M83227 Rdb:RH11153 dbSTS:STS1032 Identified using the e-PCR software (G. Schuler)"
STS	149686. .149769	/note="matching EMBL:M78784 Rdb:RH28479 dbSTS:STS4343 Identified using the e-PCR software (G. Schuler)"
STS	150104. .150262	/note="matching EMBL:T32318 Rdb:RH44093 dbSTS:STS22669 Identified using the e-PCR software (G. Schuler)"
STS	150130. .150230	/note="matching EMBL:T32325 Rdb:RH53722 dbSTS:STS15644 Identified using the e-PCR software (G. Schuler)"
STS	150720. .150944	/note="matching EMBL:W60872 Rdb:RH74933 dbSTS:STS52022 Identified using the e-PCR software (G. Schuler)"
STS	150728. .150875	/note="matching EMBL:G32230 Rdb:RH66891 dbSTS:STS46820 Identified using the e-PCR software (G. Schuler)"
STS	152309. .152430	/note="matching EMBL:AA676326 Rdb:RH104240 dbSTS:STS71769 Identified using the e-PCR software (G. Schuler)"
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STS	172947. .173063	/note="matching EMBL:D23662 Rdb:RH53814 dbSTS:STS4246 Identified using the e-PCR software (G. Schuler)"
STS	180161. .180311	/note="matching EMBL:T59873 Rdb:RH53916 dbSTS:STS20900 Identified using the e-PCR software (G. Schuler)"
STS	184269. .184418	/note="matching EMBL:H87255 Rdb:RH53526 dbSTS:STS19899

Db 15 GTTACATCCGCT 2

RESULT 13
AK027424
LOCUS AK027424 3876 bp mRNA linear PRI 15-MAY-2001
DEFINITION Homo sapiens cDNA FLJ14518 fls, clone NT2RM1000850, weakly similar
to ANKRRIN R.
ACCESSION AK027424.1 GI:14042089
VERSION AK027424.1
KEYWORDS Oligo cloning; fls (full insert sequence).
SOURCE Homo sapiens; testocarcinoma cell_line:NT2 cDNA to mRNA,
clone.lib:NT2RM1 clone:NT2RM1000850.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
REFERENCE
AUTHORS Isogai,T., Ota,T., Hayashi,K., Sugiyama,T., Otsuki,T., Suzuki,Y.,
Nishikawa,T., Nagai,K., Sugano,S., Shiratori,A., Sudo,H.,
Wagatsuma,M., Hosokiri,T., Kaku,Y., Kodaira,H., Kondo,H.,
Sugawara,M., Takahashi,M., Chida,Y., Ishida,S., Murakawa,K.,
Ono,Y., Takiguchi,S., Matanabe,S., Kimura,K., Murakami,K.,
Ishii,S., Kawai,Y., Saito,K., Yamamoto,J., Wakamatsu,A.,
Nakamura,Y., Nagahara,K., Masuko,Y., Nimomiyu,K. and Iwayanagi,T.
TITLE NEOD human cDNA sequencing project
JOURNAL Unpublished
COMMENT 2 (bases 1 to 3876)
AUTHORS Isogai,T. and Otsuki,T.
REFERENCE Direct Submission
TITLE Submitted (10-MAY-2001) Takao Isogai, Helix Research Institute,
Genomics Laboratory; 1532-3 Yama, Kisarazu, Chiba 292-0812, Japan
(E-mail:genomlab@helix.co.jp, Tel:81-438-52-3951, Fax:81-438-52-3952)
COMMENT NEOD human cDNA sequencing project supported by Ministry of
Economy, Trade and Industry of Japan; cDNA full insert sequencing;
Research Association for Biotechnology; cDNA library construction;
5' - 3' end one pass sequencing and clone selection; Helix
Research Institute (supported by Japan Key Technology Center etc.)
and Department of Virology, Institute of Medical Science,
University of Tokyo.

FEATURES
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/cell_type="testocarcinoma"
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BASE COUNT 798 a 1080 c 1186 g 812 t

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Db 140 GGAAAGGTGGGCTGGGGCTTGCGGAGGTGTACAAAGTTCGCCATGTCATCGTGA 199
Oy 132 ctacgatgtggcggtcaagatc---gttaactcgaaggcggtatccagggagggtcaggc 188
Db 200 GACTGAGTGGCTGCAATCAGTGTGCTGCGCCACGTCACGTGACGACGAGGAGCATGGA 259
Oy 189 catggaagctcgtgaatcaagaaattcgtgttcgcctagaaggaggtatagaagtgaa 248
Db 260 GCTTTTGGAAGAACCAAGCAAGATGCAATGCAATGCAATGCTTCGCTACATCTCCCTGTGA 319
Oy 249 ctggagaccaaagatcccaagccgcgcctcgtgtgaactaaattcatggaagagctccctc 308
Db 320 TGGCATCTGCCCGAAGCACTGTCGCGCTGTGTCATGAGATACATGGAACGGGCTCTGGA 379
Oy 309 ggggctgtcgtcagctccagctgcctcgcgcctgcgcctccttcgcgcctcgtgaaga 368
Db 380 AAAGCTGCTGGCTTGGAG--CCATTGCCATTGGGATCTCCGCTTCGAATCTCACGA 436
Oy 369 agtggctgttggaagtcttaactcgtcaagcagaacccgggtgctcctcagcgggaact 428
Db 437 GAGCGGCTGGGCAATGAACTTCCGACATGCAATGCAATGCAATGCAATGCAATGCAATG 496
Oy 429 caagcaccacacgctcgc 488
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Db 617 AATGCCCTACCTCCCTCCGACGACCATCAGAGGAGAGAGAGGCGGCTCCGACCAACGA 676
Oy 606 tgcagctcagctcagctcagctcagctcagctcagctcagctcagctcagctcagctc 665
Db 677 CGATGTAACGCTTGTGCAATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTG 730
Oy 666 gccaaacgaac 725
Db 731 GTTTCAGATGAGAGAACATCTCTGACATCATGATGATGATGATGATGATGATGATGATG 790
Oy 726 ggcctgagctgcccccaagccgggcctgagactcccggtctagaagagctagaaggactaa 785
Db 791 CGAGCTGCCGCCCTGTGTGAGAGCCGCCGCCGCCGCCGCCGCCGCCGCCGCCGCCCTCAT 850
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Db 851 GCACCGGTGCTGGCAGAGGAGATCCCGAGTTAGGCCACCACTTCAAGAAATTAATCTTGA 910
Oy 846 aactgataagctcctccagatggtgagaagaacaatgataagctcgtc 892
Db 911 AACGAGAGACCTGTGAAAGAACCTGATGAGCAAGTGAAGAAACTG 957

RESULT 14
LOCUS HSA278016 3879 bp mRNA linear PRI 19-NOV-2000
DEFINITION Homo sapiens mRNA for protein kinase (dlk gene).
ACCESSION AJ278016
VERSION AJ278016.1 GI:9886710
KEYWORDS dlk gene; protein kinase.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
REFERENCE 1 (bases 1 to 3879)
AUTHORS Banf,C., Rohrer,A., Stempka,I., Kincke,G., Marks,F. and

KTWLAIKSPFLHVDREHMLLEAKKMEAKFRYILPVYICREPVLYMEYMETG
SLEKILASEPLPMDLRFRILHETAVGNFELHCAAPLILDLKPNILDLAHYKIS
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BASE COUNT 825 a 1067 c 1174 g 816 t
ORIGIN

Query Match 5.98; Score 107.4; DB 9; Length 3882;
Best Local Similarity 49.18; Pred. No. 4e-16;
Matches 406; Conservative 0; Mismatches 406; Indels 15; Gaps 4;

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Db 99 GGAAGAGTGCGCTCGCGCGCTCGCGAGGTGACAGGTGCGCGCATGTCACAGAA 158
Qy 132 ctacagatgtggcggtcaagatc--gtaaactcgaagcggtatccagggaggtcaaggc 188
Db 159 GACCTGGCTGGCCATCAATGCTCGGCCAGCTGACGTGACAGCAGGAGCGCATGGA 218
Qy 189 catggcaagtcctgataacgaatccgtgttcgacctagaagggtatcagaagaagtga 248
Db 219 GCTTTGGAAAGAGCCAGAGATGAGATGAGCCAGTTTCCTACATCTCGCTCTGTA 278
Qy 249 ctgggaaccaagatcccaagcgtctcgtgtaacatcctagaagaagcgtccctgtc 308
Db 279 TGGCATGTGCGCGAAGCTGTCGGGCTGCTATGAGTACATGAGAGCGGCTCCCTGGA 338
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Job time: 4196 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 13, 2002, 21:14:38 ; Search time 24.14 Seconds
(without alignments)
525.140 Million cell updates/sec

Title: US-09-762-491-6
Perfect score: 2774
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum Db seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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38: /cgn2_6/ptodata/2/1aa/5L.COMB.pep:*
39: /cgn2_6/ptodata/2/1aa/5M.COMB.pep:*
40: /cgn2_6/ptodata/2/1aa/5N.COMB.pep:*
41: /cgn2_6/ptodata/2/1aa/5O.COMB.pep:*
42: /cgn2_6/ptodata/2/1aa/5P.COMB.pep:*
43: /cgn2_6/ptodata/2/1aa/5Q.COMB.pep:*
44: /cgn2_6/ptodata/2/1aa/5R.COMB.pep:*
45: /cgn2_6/ptodata/2/1aa/5S.COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2750	99.1	518	3	US-09-329-418-3
2	2750	99.1	518	4	US-09-329-418-3
3	2747	99.0	518	3	US-09-329-418-5
4	2747	99.0	518	4	US-09-329-418-5
5	2742	98.8	518	4	US-09-329-418-4
6	2742	98.8	518	4	US-09-329-418-4
7	2732	98.1	518	3	US-09-329-418-9
8	2722	98.1	518	4	US-09-329-418-9
9	2145.5	77.3	420	4	US-09-329-418-8
10	2145.5	77.3	420	4	US-09-329-418-8
11	1358	49.0	261	3	US-09-329-418-6
12	1358	49.0	261	4	US-09-329-418-6
13	1305	47.0	240	3	US-09-329-418-7
14	1305	47.0	240	4	US-09-329-418-7
15	445.5	16.1	656	1	US-08-444-005-15
16	445.5	16.1	656	1	US-08-444-005-15
17	423	15.2	671	4	US-09-132-118-2
18	423	15.2	671	4	US-09-132-118-2
19	407	14.7	789	1	US-08-188-930-17
20	379	13.7	531	4	US-09-069-023-1
21	379	13.7	531	4	US-09-069-023-1
22	379	13.7	540	3	US-09-019-942-1
23	379	13.7	540	4	US-09-019-942-1
24	379	13.7	540	4	US-09-069-023-27
25	376	13.6	336	4	US-09-188-930-185
26	376	13.6	336	4	US-09-099-041A-4
27	335.5	12.1	478	4	US-09-069-023-3
					Sequence 3, Appl 1
					Sequence 4, Appl 1
					Sequence 5, Appl 1
					Sequence 6, Appl 1
					Sequence 7, Appl 1
					Sequence 8, Appl 1
					Sequence 9, Appl 1
					Sequence 10, Appl 1
					Sequence 11, Appl 1
					Sequence 12, Appl 1
					Sequence 13, Appl 1
					Sequence 14, Appl 1
					Sequence 15, Appl 1
					Sequence 16, Appl 1
					Sequence 17, Appl 1
					Sequence 18, Appl 1
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					Sequence 20, Appl 1
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					Sequence 22, Appl 1
					Sequence 23, Appl 1
					Sequence 24, Appl 1
					Sequence 25, Appl 1
					Sequence 26, Appl 1
					Sequence 27, Appl 1
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					Sequence 36, Appl 1
					Sequence 37, Appl 1
					Sequence 38, Appl 1
					Sequence 39, Appl 1
					Sequence 40, Appl 1
					Sequence 41, Appl 1
					Sequence 42, Appl 1
					Sequence 43, Appl 1
					Sequence 44, Appl 1
					Sequence 45, Appl 1

28	321	11.6	264	4	US-09-069-023-7	Sequence 7, Appl 1
29	302	10.9	263	3	US-09-035-706-5	Sequence 5, Appl 1
30	302	10.9	263	4	US-08-955-841-5	Sequence 5, Appl 1
31	302	10.9	263	4	US-09-390-425-5	Sequence 5, Appl 1
32	302	10.9	821	1	US-07-928-464-2	Sequence 2, Appl 1
33	302	10.9	821	1	US-08-003-311B-2	Sequence 2, Appl 1
34	302	10.9	821	1	US-08-261-432-2	Sequence 2, Appl 1
35	302	10.9	821	5	US-08-357-533A-10	Sequence 10, Appl 1
36	290.5	10.5	513	2	US-08-459-009-10	Sequence 10, Appl 1
37	290.5	10.5	513	2	US-08-459-009-10	Sequence 10, Appl 1
38	290.5	10.5	513	3	US-08-300-584-2	Sequence 10, Appl 1
39	290.5	10.5	513	3	US-08-459-951-10	Sequence 10, Appl 1
40	290.5	10.5	513	4	US-08-738-168B-13	Sequence 13, Appl 1
41	290.5	10.5	513	4	US-08-476-123-2	Sequence 13, Appl 1
42	290.5	10.5	513	4	US-08-738-168B-5	Sequence 13, Appl 1
43	287.5	10.4	516	2	US-08-357-533A-2	Sequence 2, Appl 1
44	287.5	10.4	516	2	US-08-459-009-2	Sequence 2, Appl 1
45	287.5	10.4	516	3	US-08-459-951-2	Sequence 2, Appl 1

ALIGNMENTS

RESULT 1
US-09-329-418-3
Sequence 3, Application US-09329418
Patent No. 6096539
GENERAL INFORMATION:
APPLICANT: ZENECA Limited
TITLE OF INVENTION: PROTEIN ACTIVATOR OF APOPTOSIS
FILE REFERENCE: PHM.70516
CURRENT APPLICATION NUMBER: US/09/329,418
CURRENT FILING DATE: 1999-06-11
NUMBER OF SEQ ID NOS: 39
SOFTWARE: Fastseq for Windows Version 3.0
SEQ ID NO 3
LENGTH: 518
TYPE: PRT
ORGANISM: Homo Sapiens
US-09-329-418-3

Query Match	99.1%	Score 2750;	DB 3;	Length 518;
Best Local Similarity	99.4%	Pred. No. 1.7e-210;		
Matches 515;	Conservative 1;	Mismatches 2;	Indels 0;	Gaps 0;
Db	1	MSCVKLMPGAPAPLVISIELENOELVKGDFGTFRAOHRKCVAVAKYNSKAISRE	60	
Db	1	MSCVKLMPGAPAPLVISIELENOELVKGDFGTFRAOHRKCVAVAKYNSKAISRE	60	
Qy	61	VKMAASLDNEFTVLRLEGVIERVMDQPKALVTKRMENGSJGLQSCPPWFLCRL	120	
Db	61	VKMAASLDNEFTVLRLEGVIERVMDQPKALVTKRMENGSJGLQSCPPWFLCRL	120	
Qy	121	LKEVVGNTFYLRDQNPVLLHRDLKPSNVLPDPELVKLAIDFGISTFGGSGSGTSGEPG	180	
Db	121	LKEVVGNTFYLRDQNPVLLHRDLKPSNVLPDPELVKLAIDFGISTFGGSGSGTSGEPG	180	
Qy	181	GTGGLAPLPEFVNRKSTASDVYSFGIILMAVLAGREVELPTBESLVYAVCRORNP	240	
Db	181	GTGGLAPLPEFVNRKSTASDVYSFGIILMAVLAGREVELPTBESLVYAVCRORNP	240	
Qy	241	SLAELPQAPPEPGLEGLKELMQLCNSSEKDRPSFDECLPTDDEVFQVNNNAVST	300	
Db	241	SLAELPQAPPEPGLEGLKELMQLCNSSEKDRPSFDECLPTDDEVFQVNNNAVST	300	
Qy	301	VNDPQLQSSNRNRSIPESGSGTENDGFRRTIENQSRNDVNVSEMLNTKLTLEPPSS	360	
Db	301	VNDPQLQSSNRNRSIPESGSGTENDGFRRTIENQSRNDVNVSEMLNTKLTLEPPSS	360	
Qy	361	VPRKCSLTKRNRAGEEVQVQVATGTSSTMAQPPQETSTFRNQMPSTSTCTGTPSG	420	
Db	361	VPRKCSLTKRNRAGEEVQVQVATGTSSTMAQPPQETSTFRNQMPSTSTCTGTPSG	420	

OY 421 PRNGAEROGKMSCTPEPNPTGRPLVNTTNCSCVGVGDNNTLTMOOTALLPTMGLA 480
DB 421 PRNGAEROGKMSCTPEPNPTGRPLVNTTNCSCVGVGDNNTLTMOOTALLPTMGLA 480
OY 481 PSCKRGGLQHPPEVSGCPDPEANSPQGMVNHSGK 518
DB 481 PSCKRGGLQHPPEVSGCPDPEANSPQGMVNHSGK 518

RESULT 2

US-09-531-914-3
: Sequence 3, Application US/09531914
: Patent No. 6267956
: GENERAL INFORMATION:
: APPLICANT: ZENECA Limited
: TITLE OF INVENTION: PROTEIN ACTIVATOR OF APOPTOSIS
: FILE REFERENCE: PHM.70536
: CURRENT APPLICATION NUMBER: US/09/531.914
: PRIOR FILING DATE: 1999-06-11
: PRIOR APPLICATION NUMBER: 09/329,418
: NUMBER OF SEQ ID NOS: 39
: SOFTWARE: FASTSEQ for Windows Version 3.0
: SEQ ID NO 3
: LENGTH: 518
: TYPE: PRT
: ORGANISM: Homo Sapiens
US-09-531-914-3

Query Match 99.1%; Score 2750; DB 4; Length 518;
Best Local Similarity 99.4%; Pred. No. 1,7e-210;

Matches 515; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 MSCVILMPGAPAPLVSTIELENQELVKGDFGVRAQHRKMGYDAVKIKSKAISRE 60
DB 1 MSCVILMPGAPAPLVSTIELENQELVKGDFGVRAQHRKMGYDAVKIKSKAISRE 60
OY 61 VKAMASLDNEEVLRLBEGYIEVNNDDPKPALVTKFMENGSLSGLQSCPRPPLLCRL 120
DB 61 VKAMASLDNEEVLRLBEGYIEVNNDDPKPALVTKFMENGSLSGLQSCPRPPLLCRL 120
OY 121 LKEVILGFYLDONPVYLLHDLKPSNVLLDPDLAVKLADEFLSTFGSGSGSGEPG 180
DB 121 LKEVILGFYLDONPVYLLHDLKPSNVLLDPDLAVKLADEFLSTFGSGSGSGEPG 180
OY 181 GTLGLAPLPELVNVRKASTASDVYSGILMAVLAGREVLPTEPSLVYBAVCRNQRNP 240
DB 181 GTLGLAPLPELVNVRKASTASDVYSGILMAVLAGREVLPTEPSLVYBAVCRNQRNP 240
OY 241 SLAELPQAGPETPGLBGLKELMQLCHNSSEPRDPSFOBELPKTDEVFOYENNNAAVST 300
DB 241 SLAELPQAGPETPGLBGLKELMQLCHNSSEPRDPSFOBELPKTDEVFOYENNNAAVST 300
OY 301 VMDPISLQSSNRKRSRSTIESGCGTENDGFRRTIENHSHNDVYSEMLKLNLEPPSS 360
DB 301 VMDPISLQSSNRKRSRSTIESGCGTENDGFRRTIENHSHNDVYSEMLKLNLEPPSS 360
OY 361 VPKKPSLTKRASRAQEEVPOAMTAGTSSDSMAOPQTPETSTFRNOMPSTSTGTPSPG 420
DB 361 VPKKPSLTKRASRAQEEVPOAMTAGTSSDSMAOPQTPETSTFRNOMPSTSTGTPSPG 420
OY 421 PRNGAEROGKMSCTPEPNPTGRPLVNTTNCSCVGVGDNNTLTMOOTALLPTMGLA 480
DB 421 PRNGAEROGKMSCTPEPNPTGRPLVNTTNCSCVGVGDNNTLTMOOTALLPTMGLA 480
OY 481 PSCKRGGLQHPPEVSGCPDPEANSPQGMVNHSGK 518
DB 481 PSCKRGGLQHPPEVSGCPDPEANSPQGMVNHSGK 518

RESULT 3

US-09-329-418-5
: Sequence 5, Application US/09329418
: Patent No. 6096539
: GENERAL INFORMATION:
: APPLICANT: ZENECA Limited
: TITLE OF INVENTION: PROTEIN ACTIVATOR OF APOPTOSIS
: FILE REFERENCE: PHM.70536
: CURRENT APPLICATION NUMBER: US/09/329,418
: PRIOR FILING DATE: 1999-06-11
: NUMBER OF SEQ ID NOS: 39
: SOFTWARE: FASTSEQ for Windows Version 3.0
: SEQ ID NO 5
: LENGTH: 518
: TYPE: PRT
: ORGANISM: Dactylolaccal Sequence
: FEATURE:
: OTHER INFORMATION: Dominant Negative Mutant Embodiment
US-09-329-418-5

Query Match 99.0%; Score 2747; DB 3; Length 518;
Best Local Similarity 99.2%; Pred. No. 2,9e-210;

Matches 514; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 1 MSCVILMPGAPAPLVSTIELENQELVKGDFGVRAQHRKMGYDAVKIKSKAISRE 60
DB 1 MSCVILMPGAPAPLVSTIELENQELVKGDFGVRAQHRKMGYDAVKIKSKAISRE 60
OY 61 VKAMASLDNEEVLRLBEGYIEVNNDDPKPALVTKFMENGSLSGLQSCPRPPLLCRL 120
DB 61 VKAMASLDNEEVLRLBEGYIEVNNDDPKPALVTKFMENGSLSGLQSCPRPPLLCRL 120
OY 121 LKEVILGFYLDONPVYLLHDLKPSNVLLDPDLAVKLADEFLSTFGSGSGSGEPG 180
DB 121 LKEVILGFYLDONPVYLLHDLKPSNVLLDPDLAVKLADEFLSTFGSGSGSGEPG 180
OY 181 GTLGLAPLPELVNVRKASTASDVYSGILMAVLAGREVLPTEPSLVYBAVCRNQRNP 240
DB 181 GTLGLAPLPELVNVRKASTASDVYSGILMAVLAGREVLPTEPSLVYBAVCRNQRNP 240
OY 241 SLAELPQAGPETPGLBGLKELMQLCHNSSEPRDPSFOBELPKTDEVFOYENNNAAVST 300
DB 241 SLAELPQAGPETPGLBGLKELMQLCHNSSEPRDPSFOBELPKTDEVFOYENNNAAVST 300
OY 301 VMDPISLQSSNRKRSRSTIESGCGTENDGFRRTIENHSHNDVYSEMLKLNLEPPSS 360
DB 301 VMDPISLQSSNRKRSRSTIESGCGTENDGFRRTIENHSHNDVYSEMLKLNLEPPSS 360
OY 361 VPKKPSLTKRASRAQEEVPOAMTAGTSSDSMAOPQTPETSTFRNOMPSTSTGTPSPG 420
DB 361 VPKKPSLTKRASRAQEEVPOAMTAGTSSDSMAOPQTPETSTFRNOMPSTSTGTPSPG 420
OY 421 PRNGAEROGKMSCTPEPNPTGRPLVNTTNCSCVGVGDNNTLTMOOTALLPTMGLA 480
DB 421 PRNGAEROGKMSCTPEPNPTGRPLVNTTNCSCVGVGDNNTLTMOOTALLPTMGLA 480
OY 481 PSCKRGGLQHPPEVSGCPDPEANSPQGMVNHSGK 518
DB 481 PSCKRGGLQHPPEVSGCPDPEANSPQGMVNHSGK 518

RESULT 4

US-09-531-914-5
: Sequence 5, Application US/09531914
: Patent No. 6267956
: GENERAL INFORMATION:
: APPLICANT: ZENECA Limited
: TITLE OF INVENTION: PROTEIN ACTIVATOR OF APOPTOSIS
: FILE REFERENCE: PHM.70536
: CURRENT APPLICATION NUMBER: US/09/531.914
: PRIOR FILING DATE: 1999-06-11

NUMBER OF SEQ ID NOS: 39
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 5
LENGTH: 518
TYPE: PR
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Dominant Negative Mutant Embodiment
US-09-531-914-5

Query Match 99.0%; Score 2747; DB 4; Length 518;
Best Local Similarity 99.2%; Pred. No. 2,96-210;
Matches 514; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

1 MSCVRLPAGAPAPLVSTIELENOELVKGDFGTVFRAOHRKMGIDVAIVNSKAISSRE 60
1 MSCVRLPAGAPAPLVSTIELENOELVKGDFGTVFRAOHRKMGIDVAIVNSKAISSRE 60
61 VKAASLQNEFVRLBCEVIEKVMNDPDPALVTKFMENGLSGILSQCPRPMLLCRL 120
61 VKAASLQNEFVRLBCEVIEKVMNDPDPALVTKFMENGLSGILSQCPRPMLLCRL 120
121 LKEVYLGAFYLDQNPVTLHRDLKPSNVLPDELVKYLADGLSTFGGSGSGSGEPG 180
121 LKEVYLGAFYLDQNPVTLHRDLKPSNVLPDELVKYLADGLSTFGGSGSGSGEPG 180
181 GTLGYLAPLEFVNNRKAASADVTSFGILMAVLAGREVELPTEPSLYEAVCNQNRP 240
181 GTLGYLAPLEFVNNRKAASADVTSFGILMAVLAGREVELPTEPSLYEAVCNQNRP 240
181 GTLGYLAPLEFVNNRKAASADVTSFGILMAVLAGREVELPTEPSLYEAVCNQNRP 240
241 SLATLPAGPETPCLBCKELMQLCNSSEPKDRPSFOCLPKTDEVOMENNNNAVST 300
241 SLATLPAGPETPCLBCKELMQLCNSSEPKDRPSFOCLPKTDEVOMENNNNAVST 300
301 VKDLSQLKSSNRRTSIPESGCGTEMDGFRRTIENQHSRDVAVSEKLNKLNLEEPS 360
301 VKDLSQLKSSNRRTSIPESGCGTEMDGFRRTIENQHSRDVAVSEKLNKLNLEEPS 360
361 VPKCPSLTKRSRAOEVOVPOANTACTSSDMAOPOTPETSTRNOMPSTSTGTPSPG 420
361 VPKCPSLTKRSRAOEVOVPOANTACTSSDMAOPOTPETSTRNOMPSTSTGTPSPG 420
421 PRGNGAEROGAMNSCRTPENPVYGRPLVNTYNCSSGVQVGDNNYLTMOQTALPTMGLA 480
421 PRGNGAEROGAMNSCRTPENPVYGRPLVNTYNCSSGVQVGDNNYLTMOQTALPTMGLA 480
481 PSKGRGLQHPPPVGSQEGPKDPEANSPQGYNHSGR 518
481 PSKGRGLQHPPPVGSQEGPKDPEANSPQGYNHSGR 518

RESULT 5
US-09-329-418-4
Sequence 4, Application US/09329418
Patent No. 6096539
GENERAL INFORMATION:
APPLICANT: ZENECA Limited
TITLE OF INVENTION: PROTEIN ACTIVATOR OF APOPTOSIS
FILE REFERENCE: PHM.70536
CURRENT APPLICATION NUMBER: US/09/329,418
CURRENT FILING DATE: 1999-06-11
NUMBER OF SEQ ID NOS: 39
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 4
LENGTH: 518
TYPE: PR
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Dominant Negative Mutant Embodiment
US-09-329-418-4

Query Match 98.8%; Score 2742; DB 3; Length 518;
Best Local Similarity 99.2%; Pred. No. 7,36-210;
Matches 514; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

1 MSCVRLPAGAPAPLVSTIELENOELVKGDFGTVFRAOHRKMGIDVAIVNSKAISSRE 60
1 MSCVRLPAGAPAPLVSTIELENOELVKGDFGTVFRAOHRKMGIDVAIVNSKAISSRE 60
61 VKAASLQNEFVRLBCEVIEKVMNDPDPALVTKFMENGLSGILSQCPRPMLLCRL 120
61 VKAASLQNEFVRLBCEVIEKVMNDPDPALVTKFMENGLSGILSQCPRPMLLCRL 120
121 LKEVYLGAFYLDQNPVTLHRDLKPSNVLPDELVKYLADGLSTFGGSGSGSGEPG 180
121 LKEVYLGAFYLDQNPVTLHRDLKPSNVLPDELVKYLADGLSTFGGSGSGSGEPG 180
181 GTLGYLAPLEFVNNRKAASADVTSFGILMAVLAGREVELPTEPSLYEAVCNQNRP 240
181 GTLGYLAPLEFVNNRKAASADVTSFGILMAVLAGREVELPTEPSLYEAVCNQNRP 240
241 SLATLPAGPETPCLBCKELMQLCNSSEPKDRPSFOCLPKTDEVOMENNNNAVST 300
241 SLATLPAGPETPCLBCKELMQLCNSSEPKDRPSFOCLPKTDEVOMENNNNAVST 300
301 VKDLSQLKSSNRRTSIPESGCGTEMDGFRRTIENQHSRDVAVSEKLNKLNLEEPS 360
301 VKDLSQLKSSNRRTSIPESGCGTEMDGFRRTIENQHSRDVAVSEKLNKLNLEEPS 360
361 VPKCPSLTKRSRAOEVOVPOANTACTSSDMAOPOTPETSTRNOMPSTSTGTPSPG 420
361 VPKCPSLTKRSRAOEVOVPOANTACTSSDMAOPOTPETSTRNOMPSTSTGTPSPG 420
421 PRGNGAEROGAMNSCRTPENPVYGRPLVNTYNCSSGVQVGDNNYLTMOQTALPTMGLA 480
421 PRGNGAEROGAMNSCRTPENPVYGRPLVNTYNCSSGVQVGDNNYLTMOQTALPTMGLA 480
481 PSKGRGLQHPPPVGSQEGPKDPEANSPQGYNHSGR 518
481 PSKGRGLQHPPPVGSQEGPKDPEANSPQGYNHSGR 518

RESULT 6
US-09-531-914-4
Sequence 4, Application US/09531914
Patent No. 6267956
GENERAL INFORMATION:
APPLICANT: ZENECA Limited
TITLE OF INVENTION: PROTEIN ACTIVATOR OF APOPTOSIS
FILE REFERENCE: PHM.70536
CURRENT APPLICATION NUMBER: US/09/531,914
CURRENT FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 09/329,418
NUMBER OF SEQ ID NOS: 39
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 4
LENGTH: 518
TYPE: PR
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Dominant Negative Mutant Embodiment
US-09-531-914-4

Query Match 98.8%; Score 2742; DB 4; Length 518;
Best Local Similarity 99.2%; Pred. No. 7,36-210;
Matches 514; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

1 MSCVRLPAGAPAPLVSTIELENOELVKGDFGTVFRAOHRKMGIDVAIVNSKAISSRE 60
1 MSCVRLPAGAPAPLVSTIELENOELVKGDFGTVFRAOHRKMGIDVAIVNSKAISSRE 60
61 VKAASLQNEFVRLBCEVIEKVMNDPDPALVTKFMENGLSGILSQCPRPMLLCRL 120

DB 61 VKAASLDNEFYLRLEGVIERKVMDDPKPALVTKFKMENGSLGILQSCPRPMLICRL 120
QY 121 LKEVYLGMEFYLRHLDONPVYLHRLDKPSNVLPDELYHVKLADGSLTPOGSGSGSGSGE 180
DB 122 LKEVYLGMEFYLRHLDONPVYLHRLDKPSNVLPDELYHVKLADGSLTPOGSGSGSGSGE 180
QY 181 GTLGTLAPELPVYNNRKAASDVYSFGILMAVLAGREVELPTEPSLYEAVCNQRNP 240
DB 181 GTLGTLAPELPVYNNRKAASDVYSFGILMAVLAGREVELPTEPSLYEAVCNQRNP 240
QY 241 SLAEIPQAGPETPGLEGKELMQLCWSSEPRDRSPFOECLPKTDEVFOYENNNNAVST 300
DB 241 SLAEIPQAGPETPGLEGKELMQLCWSSEPRDRSPFOECLPKTDEVFOYENNNNAVST 300
QY 301 VDFLSQLKSSNRFRSIPESGOGGTENDGFRRTIENHSHNDVYSEMLKLNLEPPSS 360
DB 301 VDFLSQLKSSNRFRSIPESGOGGTENDGFRRTIENHSHNDVYSEMLKLNLEPPSS 360
QY 361 VPKKCPSLTKRSRAQEQVPOAWTACTSSDSMAOPOTETSTFRNOMPSTSTGTPSPG 420
DB 361 VPKKCPSLTKRSRAQEQVPOAWTACTSSDSMAOPOTETSTFRNOMPSTSTGTPSPG 420
QY 421 PRGNQCAEROGMNSCRTPEDPNVTGRPLVNIYNCSCVOYGDNNYLTMOQTALPTMGLA 480
DB 421 PRGNQCAEROGMNSCRTPEDPNVTGRPLVNIYNCSCVOYGDNNYLTMOQTALPTMGLA 480
QY 481 PSGRGRLQHPPPVGSQBPDPKDPAMSRPOGMYNHSGK 518
DB 481 PSGRGRLQHPPPVGSQBPDPKDPAMSRPOGMYNHSGK 518

RESULT 7

US-09-329-418-9
Sequence 9, Application US/09329418
Patent No. 6098539
GENERAL INFORMATION:
APPLICANT: ZENECA Limited
TITLE OF INVENTION: PROTEIN ACTIVATOR OF APOPTOSIS
FILE REFERENCE: PHM.70536
CURRENT APPLICATION NUMBER: US/09/329,418
CURRENT FILING DATE: 1999-06-11
NUMBER OF SEQ ID NOS: 39
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 9
LENGTH: 518
TYPE: PRP
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Dominant Negative Mutant Embodiment
US-09-329-418-9

Query Match

Best Local Similarity 98.1%; Score 2722; DB 3; Length 518;
Matches 513; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 MSCVKLMPSCGAPLVSIELENOELVGKDGCTVFRQHRKMGDYAVAKIVNSKASIRE 60
DB 1 MSCVKLMPSCGAPLVSIELENOELVGKDGCTVFRQHRKMGDYAVAKIVNSKASIRE 60
QY 61 VKAASLDNEFYLRLEGVIERKVMDDPKPALVTKFKMENGSLGILQSCPRPMLICRL 120
DB 61 VKAASLDNEFYLRLEGVIERKVMDDPKPALVTKFKMENGSLGILQSCPRPMLICRL 120
QY 121 LKEVYLGMEFYLRHLDONPVYLHRLDKPSNVLPDELYHVKLADGSLTPOGSGSGSGE 180
DB 121 LKEVYLGMEFYLRHLDONPVYLHRLDKPSNVLPDELYHVKLADGSLTPOGSGSGSGE 180
QY 181 GTLGTLAPELPVYNNRKAASDVYSFGILMAVLAGREVELPTEPSLYEAVCNQRNP 240
DB 181 GTLGTLAPELPVYNNRKAASDVYSFGILMAVLAGREVELPTEPSLYEAVCNQRNP 240

QY 241 SLAEIPQAGPETPGLEGKELMQLCWSSEPRDRSPFOECLPKTDEVFOYENNNNAVST 300
DB 241 SLAEIPQAGPETPGLEGKELMQLCWSSEPRDRSPFOECLPKTDEVFOYENNNNAVST 300
QY 301 VDFLSQLKSSNRFRSIPESGOGGTENDGFRRTIENHSHNDVYSEMLKLNLEPPSS 360
DB 301 VDFLSQLKSSNRFRSIPESGOGGTENDGFRRTIENHSHNDVYSEMLKLNLEPPSS 360
QY 361 VPKKCPSLTKRSRAQEQVPOAWTACTSSDSMAOPOTETSTFRNOMPSTSTGTPSPG 420
DB 361 VPKKCPSLTKRSRAQEQVPOAWTACTSSDSMAOPOTETSTFRNOMPSTSTGTPSPG 420
QY 421 PRGNQCAEROGMNSCRTPEDPNVTGRPLVNIYNCSCVOYGDNNYLTMOQTALPTMGLA 480
DB 421 PRGNQCAEROGMNSCRTPEDPNVTGRPLVNIYNCSCVOYGDNNYLTMOQTALPTMGLA 480
QY 481 PSGRGRLQHPPPVGSQBPDPKDPAMSRPOGMYNHSGK 518
DB 481 PSGRGRLQHPPPVGSQBPDPKDPAMSRPOGMYNHSGK 518

RESULT 8

US-09-531-914-9
Sequence 9, Application US/09531914
Patent No. 6267956
GENERAL INFORMATION:
APPLICANT: ZENECA Limited
TITLE OF INVENTION: PROTEIN ACTIVATOR OF APOPTOSIS
FILE REFERENCE: PHM.70536
CURRENT APPLICATION NUMBER: US/09/531,914
CURRENT FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 09/329,418
NUMBER OF SEQ ID NOS: 39
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 9
LENGTH: 518
TYPE: PRP
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Dominant Negative Mutant Embodiment
US-09-531-914-9

Query Match 98.1%; Score 2722; DB 4; Length 518;
Best Local Similarity 99.0%; Pred. No. 2,8e-208;
Matches 513; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 MSCVKLMPSCGAPLVSIELENOELVGKDGCTVFRQHRKMGDYAVAKIVNSKASIRE 60
DB 1 MSCVKLMPSCGAPLVSIELENOELVGKDGCTVFRQHRKMGDYAVAKIVNSKASIRE 60
QY 61 VKAASLDNEFYLRLEGVIERKVMDDPKPALVTKFKMENGSLGILQSCPRPMLICRL 120
DB 61 VKAASLDNEFYLRLEGVIERKVMDDPKPALVTKFKMENGSLGILQSCPRPMLICRL 120
QY 121 LKEVYLGMEFYLRHLDONPVYLHRLDKPSNVLPDELYHVKLADGSLTPOGSGSGSGE 180
DB 121 LKEVYLGMEFYLRHLDONPVYLHRLDKPSNVLPDELYHVKLADGSLTPOGSGSGSGE 180
QY 181 GTLGTLAPELPVYNNRKAASDVYSFGILMAVLAGREVELPTEPSLYEAVCNQRNP 240
DB 181 GTLGTLAPELPVYNNRKAASDVYSFGILMAVLAGREVELPTEPSLYEAVCNQRNP 240
QY 241 SLAEIPQAGPETPGLEGKELMQLCWSSEPRDRSPFOECLPKTDEVFOYENNNNAVST 300
DB 241 SLAEIPQAGPETPGLEGKELMQLCWSSEPRDRSPFOECLPKTDEVFOYENNNNAVST 300
QY 301 VDFLSQLKSSNRFRSIPESGOGGTENDGFRRTIENHSHNDVYSEMLKLNLEPPSS 360
DB 301 VDFLSQLKSSNRFRSIPESGOGGTENDGFRRTIENHSHNDVYSEMLKLNLEPPSS 360
QY 361 VPKKCPSLTKRSRAQEQVPOAWTACTSSDSMAOPOTETSTFRNOMPSTSTGTPSPG 420
DB 361 VPKKCPSLTKRSRAQEQVPOAWTACTSSDSMAOPOTETSTFRNOMPSTSTGTPSPG 420

```

DB 361 VPKKCSLTKRRRAOEEOVPOAMTAGTSSDMAOPPTPETSTFRNOMPSPTSTGTPSPG 420
OY 421 PRNGOAEKOGNMSGRTPEPPATGRLVYVNCSCVGDNNYITMOTALTATKLA 480
DB 422 PRNGOAEKOGNMSGRTPEPPATGRLVYVNCSCVGDNNYITMOTALTATKLA 480
OY 481 PSCKGKGLHPPVGSQSGPDPPEANSHPOGWTNHSK 518
DB 481 PSCKGKGLHPPVGSQSGPDPPEANSHPOGWTNHSK 518

```

RESULT 9

```

US-09-329-418-8
; Sequence 8, Application US/09329418
; Patent No. 6096539
; GENERAL INFORMATION:
; APPLICANT: ZENCA Limited
; TITLE OF INVENTION: PROTEIN ACTIVATOR OF APOPTOSIS
; PIR REFERENCE: PHM.70536
; CURRENT APPLICATION NUMBER: US/09/329,418
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 8
; LENGTH: 420
; TYPE: PRP
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Delta Death Domain
US-09-329-418-8

```

```

Query Match 77.3%; Score 2145.5; DB 3; Length 420;
Best Local Similarity 98.3%; Pred. No. 1.3e-162;
Matches 413; Conservative 1; Mismatches 5; Indels 1; Gaps 1;

```

```

OY 1 MSCVTLMPGAPAPLYSTIELENOELVKGDFGTPRAOHRKGVAVKYNKATLSRE 60
DB 1 MSCVTLMPGAPAPLYSTIELENOELVKGDFGTPRAOHRKGVAVKYNKATLSRE 60
OY 61 VKAMSLDNEFVLRLEGYIEKVN-DODPRPALVTKFMENGSLGILASQCPRPPLLCR 119
DB 61 VKAMSLDNEFVLRLEGYIEKVN-DODPRPALVTKFMENGSLGILASQCPRPPLLCR 119
OY 120 LKEVYLGMEFYLDHONPVLRLRDLKPSNVLPEDELHVKLADFGSLTFPGGSGSGTSGSEP 179
DB 120 LKEVYLGMEFYLDHONPVLRLRDLKPSNVLPEDELHVKLADFGSLTFPGGSGSGTSGSEP 179
OY 121 LKEVYLGMEFYLDHONPVLRLRDLKPSNVLPEDELHVKLADFGSLTFPGGSGSGTSGSEP 180
DB 121 LKEVYLGMEFYLDHONPVLRLRDLKPSNVLPEDELHVKLADFGSLTFPGGSGSGTSGSEP 180
OY 180 GGTGCTYLAPELFVNNRRASTASDVTSFGILMAVYLAGREVELPEPSLYEVANCNQR 239
DB 180 GGTGCTYLAPELFVNNRRASTASDVTSFGILMAVYLAGREVELPEPSLYEVANCNQR 239
OY 240 PSIAELPQAGPETPGLGELKELMQLCWSSEPKDRPSFOCLPRTDEVQVYENNNAAVS 299
DB 240 PSIAELPQAGPETPGLGELKELMQLCWSSEPKDRPSFOCLPRTDEVQVYENNNAAVS 299
OY 300 TVKDFLSQKSSNRFRSIPESGCGTDMOGFRTIENQSRNDVAVSEMLKLNLEPPS 359
DB 300 TVKDFLSQKSSNRFRSIPESGCGTDMOGFRTIENQSRNDVAVSEMLKLNLEPPS 359
OY 360 SVPKKCSLTKRRRAOEEOVPOAMTAGTSSDMAOPPTPETSTFRNOMPSPTSTGTPSP 419
DB 360 SVPKKCSLTKRRRAOEEOVPOAMTAGTSSDMAOPPTPETSTFRNOMPSPTSTGTPSP 419
OY 361 SVPKKCSLTKRRRAOEEOVPOAMTAGTSSDMAOPPTPETSTFRNOMPSPTSTGTPSP 420
DB 361 SVPKKCSLTKRRRAOEEOVPOAMTAGTSSDMAOPPTPETSTFRNOMPSPTSTGTPSP 420

```

RESULT 10

```

US-09-531-914-8
; Sequence 8, Application US/09331914
; Patent No. 6267936
; GENERAL INFORMATION:
; APPLICANT: ZENCA Limited
; TITLE OF INVENTION: PROTEIN ACTIVATOR OF APOPTOSIS

```

```

; FILE REFERENCE: PHM.70536
; CURRENT APPLICATION NUMBER: US/09/531,914
; CURRENT FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 09/329,418
; PRIOR FILING DATE: 1999-06-11
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 8
; LENGTH: 420
; TYPE: PRP
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Delta Death Domain
US-09-531-914-8

```

```

Query Match 77.3%; Score 2145.5; DB 4; Length 420;
Best Local Similarity 98.3%; Pred. No. 1.3e-162;
Matches 413; Conservative 1; Mismatches 5; Indels 1; Gaps 1;

```

```

OY 1 MSCVTLMPGAPAPLYSTIELENOELVKGDFGTPRAOHRKGVAVKYNKATLSRE 60
DB 1 MSCVTLMPGAPAPLYSTIELENOELVKGDFGTPRAOHRKGVAVKYNKATLSRE 60
OY 61 VKAMSLDNEFVLRLEGYIEKVN-DODPRPALVTKFMENGSLGILASQCPRPPLLCR 119
DB 61 VKAMSLDNEFVLRLEGYIEKVN-DODPRPALVTKFMENGSLGILASQCPRPPLLCR 119
OY 120 LKEVYLGMEFYLDHONPVLRLRDLKPSNVLPEDELHVKLADFGSLTFPGGSGSGTSGSEP 179
DB 120 LKEVYLGMEFYLDHONPVLRLRDLKPSNVLPEDELHVKLADFGSLTFPGGSGSGTSGSEP 179
OY 121 LKEVYLGMEFYLDHONPVLRLRDLKPSNVLPEDELHVKLADFGSLTFPGGSGSGTSGSEP 180
DB 121 LKEVYLGMEFYLDHONPVLRLRDLKPSNVLPEDELHVKLADFGSLTFPGGSGSGTSGSEP 180
OY 180 GGTGCTYLAPELFVNNRRASTASDVTSFGILMAVYLAGREVELPEPSLYEVANCNQR 239
DB 180 GGTGCTYLAPELFVNNRRASTASDVTSFGILMAVYLAGREVELPEPSLYEVANCNQR 239
OY 240 PSIAELPQAGPETPGLGELKELMQLCWSSEPKDRPSFOCLPRTDEVQVYENNNAAVS 299
DB 240 PSIAELPQAGPETPGLGELKELMQLCWSSEPKDRPSFOCLPRTDEVQVYENNNAAVS 299
OY 300 TVKDFLSQKSSNRFRSIPESGCGTDMOGFRTIENQSRNDVAVSEMLKLNLEPPS 359
DB 300 TVKDFLSQKSSNRFRSIPESGCGTDMOGFRTIENQSRNDVAVSEMLKLNLEPPS 359
OY 360 SVPKKCSLTKRRRAOEEOVPOAMTAGTSSDMAOPPTPETSTFRNOMPSPTSTGTPSP 419
DB 360 SVPKKCSLTKRRRAOEEOVPOAMTAGTSSDMAOPPTPETSTFRNOMPSPTSTGTPSP 419
OY 361 SVPKKCSLTKRRRAOEEOVPOAMTAGTSSDMAOPPTPETSTFRNOMPSPTSTGTPSP 420
DB 361 SVPKKCSLTKRRRAOEEOVPOAMTAGTSSDMAOPPTPETSTFRNOMPSPTSTGTPSP 420

```

RESULT 11

```

US-09-329-418-6
; Sequence 6, Application US/09329418
; Patent No. 6096539
; GENERAL INFORMATION:
; APPLICANT: ZENCA Limited
; TITLE OF INVENTION: PROTEIN ACTIVATOR OF APOPTOSIS
; FILE REFERENCE: PHM.70536
; CURRENT APPLICATION NUMBER: US/09/329,418
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 261
; TYPE: PRP
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Kinase Domain
US-09-329-418-6

```

```

Query Match 49.0%; Score 1358; DB 3; Length 261;
Best Local Similarity 99.3%; Pred. No. 2.4e-100;
Matches 259; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```



```
QY 21 LENGLVKGDFGTFVPAORHKGVDYAVKIVSKAISREYKAMASLDNEEVLLEGVIE 80
D 1 LENGLVKGDFGTFVPAORHKGVDYAVKIVSKAISREYKAMASLDNEEVLLEGVIE 60
QY 81 KYMNDOPKALVTKFENGSLGSLQSCPPRPWLLCRLKEVVLGKFFYLHDONPVLLH 140
D 61 KYMNDOPKALVTKFENGSLGSLQSCPPRPWLLCRLKEVVLGKFFYLHDONPVLLH 120
QY 141 RDLKPSVNLDPDLHVLADFGSLTFQSGSGSGTSGSGEPGCTIGYLADELFEVNNRKA 200
D 121 RDLKPSVNLDPDLHVLADFGSLTFQSGSGSGTSGSGEPGCTIGYLADELFEVNNRKA 180
QY 201 ASDVYSFGILMMNAVLAGREVELPTPESLYVEAVCNRONRPSLAELPOAGPETPELE 260
D 181 ASDVYSFGILMMNAVLAGREVELPTPESLYVEAVCNRONRPSLAELPOAGPETPELE 240
QY 261 LMOLCMSSEPRDRPSFOECLP 281
D 241 LMOLCMSSEPRDRPSFOECLP 261

RESULT 12
US-09-531-914-6
; Sequence 6, Application US/09531914
; Patent No. 6267956
; GENERAL INFORMATION:
; APPLICANT: ZENECA Limited
; TITLE OF INVENTION: PROTEIN ACTIVATOR OF APOPTOSIS
; FILE REFERENCE: PHM.70536
; CURRENT APPLICATION NUMBER: US/09/531,914
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 09/329,418
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 261
; TYPE: PRP
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Kinase Domain
US-09-531-914-6

Query Match 49.0%; Score 1358; DB 4; Length 261;
Best Local Similarity 99.2%; Pred. No. 2,46-100;
Matches 259; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 21 LENGLVKGDFGTFVPAORHKGVDYAVKIVSKAISREYKAMASLDNEEVLLEGVIE 80
D 1 LENGLVKGDFGTFVPAORHKGVDYAVKIVSKAISREYKAMASLDNEEVLLEGVIE 60
QY 81 KYMNDOPKALVTKFENGSLGSLQSCPPRPWLLCRLKEVVLGKFFYLHDONPVLLH 140
D 61 KYMNDOPKALVTKFENGSLGSLQSCPPRPWLLCRLKEVVLGKFFYLHDONPVLLH 120
QY 141 RDLKPSVNLDPDLHVLADFGSLTFQSGSGSGTSGSGEPGCTIGYLADELFEVNNRKA 200
D 121 RDLKPSVNLDPDLHVLADFGSLTFQSGSGSGTSGSGEPGCTIGYLADELFEVNNRKA 180
QY 201 ASDVYSFGILMMNAVLAGREVELPTPESLYVEAVCNRONRPSLAELPOAGPETPELE 260
D 181 ASDVYSFGILMMNAVLAGREVELPTPESLYVEAVCNRONRPSLAELPOAGPETPELE 240
QY 261 LMOLCMSSEPRDRPSFOECLP 281
D 241 LMOLCMSSEPRDRPSFOECLP 261

RESULT 13
US-09-329-418-7
; Sequence 7, Application US/09329418
```

```
; Patent No. 6096539
; GENERAL INFORMATION:
; APPLICANT: ZENECA Limited
; TITLE OF INVENTION: PROTEIN ACTIVATOR OF APOPTOSIS
; FILE REFERENCE: PHM.70536
; CURRENT APPLICATION NUMBER: US/09/329,418
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 240
; TYPE: PRP
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Death Domain
US-09-329-418-7

Query Match 47.0%; Score 1305; DB 3; Length 240;
Best Local Similarity 99.6%; Pred. No. 3,46-96;
Matches 239; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 279 CLPKTDEVFOVNNNAAVSTVKDFLSQLKSSNRRFSIPESGGGTENDGFRRTIENH 338
D 1 CLPKTDEVFOVNNNAAVSTVKDFLSQLKSSNRRFSIPESGGGTENDGFRRTIENH 60
QY 339 SRNDVASEMLKNTLNEEPSSVPRKCPSLTRRSRAOEDVPOAMTAGTSSDSNAQPOT 398
D 61 SRNDVASEMLKNTLNEEPSSVPRKCPSLTRRSRAOEDVPOAMTAGTSSDSNAQPOT 120
QY 459 OYGDNNYLTMOQTALPTMGLAPSGKRGLOHPPVGSOECPKPEASRPOGMYNRSGK 518
D 181 OYGDNNYLTMOQTALPTMGLAPSGKRGLOHPPVGSOECPKPEASRPOGMYNRSGK 240

RESULT 14
US-09-531-914-7
; Sequence 7, Application US/09531914
; Patent No. 6267956
; GENERAL INFORMATION:
; APPLICANT: ZENECA Limited
; TITLE OF INVENTION: PROTEIN ACTIVATOR OF APOPTOSIS
; FILE REFERENCE: PHM.70536
; CURRENT APPLICATION NUMBER: US/09/531,914
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 09/329,418
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 240
; TYPE: PRP
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Death Domain
US-09-531-914-7

Query Match 47.0%; Score 1305; DB 4; Length 240;
Best Local Similarity 99.6%; Pred. No. 3,46-96;
Matches 239; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 279 CLPKTDEVFOVNNNAAVSTVKDFLSQLKSSNRRFSIPESGGGTENDGFRRTIENH 338
D 1 CLPKTDEVFOVNNNAAVSTVKDFLSQLKSSNRRFSIPESGGGTENDGFRRTIENH 60
QY 339 SRNDVASEMLKNTLNEEPSSVPRKCPSLTRRSRAOEDVPOAMTAGTSSDSNAQPOT 398
D 61 SRNDVASEMLKNTLNEEPSSVPRKCPSLTRRSRAOEDVPOAMTAGTSSDSNAQPOT 120
```

QY 399 PETSTRNOMSPSTGTGPPSPGRNGAEROGNMNSCTPEPNVYGRPLVNTYNSGV 438
DB 121 PETSTRNOMSPSTGTGPPSPGRNGAEROGNMNSCTPEPNVYGRPLVNTYNSGV 180
QY 459 QVGDNNYITMOTTTALPTWGLAPSGKRGLOHPPPVSGQEGKDEPANSRPOGYNHSGR 518
DB 181 QVGDNNYITMOTTTALPTWGLAPSGKRGLOHPPPVSGQEGKDEPANSRPOGYNHSGR 240

RESULT 15

US-08-444-005-15

Sequence 15, Application us/08444005

Patent No 5674734

GENERAL INFORMATION:

APPLICANT: Leder, Philip

APPLICANT: Seed, Brian

APPLICANT: Stanger, Ben Z.

APPLICANT: Lee, Tae-Ho

APPLICANT: Kim, Emily

TITLE OF INVENTION: CELL DEATH PROTEIN

NUMBER OF SEQUENCES: 35

CORRESPONDENCE ADDRESS:

ADDRESSEE: Fish & Richardson P.C.

STREET: 225 Franklin Street, Suite 3100

CITY: Boston

STATE: MA

COUNTRY: USA

ZIP: 02110-2804

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/444,005

FILING DATE:

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Clark, Paul T.

REGISTRATION NUMBER: 30,164

REFERENCE/DOCKET NUMBER: 00383/026001

TELECOMMUNICATION INFORMATION:

TELEPHONE: 617/542-5070

TELEFAX: 617/542-8906

TELEX: 200154

INFORMATION FOR SEQ ID NO: 15:

SEQUENCE CHARACTERISTICS:

LENGTH: 656 amino acids

TYPE: amino acid

STRANDEDNESS: not relevant

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-444-005-15

Query Match 15.18; Score 445.5; DB 1; Length 656;

Best local similarity 26.28; Pred. No. 2,3e-27;

Matches 158; Conservative 89; Mismatches 205; Indels 151; Gaps 23;

QY 15 LVSTEELEMOELVKGDFGVFRQHRKMGYDAVAVIVN-----SKAISREYKAMASL 67
DB 12 MASSDLLEKTL-DSGGFGKVSCLTIRSHQFVILKVVYGPRAEYNEVLLSECKMHRRL 70
QY 68 DNEFVLRLEG-VIEKVMDDOPKALVYTRFMENGSISGLLOSQCRPMPVLCRLKREVL 126
DB 71 RRSRVVRLGLIIIEGNY-----SLVMEYMEKGNLMHVLKQIDIVPLSLKGRIVYPAIE 124
QY 127 GMFYLDQNPVTLRLDLKPSVYLPDEPLHVKLADPGLSTFGGSGO-----SGT 174
DB 125 GNCYLDHG--VIRKDKPERILVDQFHKIADLGVASFRTWSKLTREKDNKQREYSS 182
QY 175 GSGEPGLIGYLALELVFNVRKRASTASDVYSPGLIMAVLAGREVELPTEPSIYEAVC 234

DB 183 TKNNKGLITIMAEHNDINAKPTKSDVYSGYIVMAIFAKR---PYE-----NVIC 234
QY 235 NNO-----NRSLABLPOAGPEYTPGLDKELMQLCWSEPKDRSF---QECLEPK 282
DB 235 TQPIYICIKSGRRPVEVILEYCPRE---IISLMERCWQAIPEDRPTFLGIEEPRPF 289
QY 283 TDEVF-QVVENMMAAVSTVADFLSOLKSNRRFS-----IPES----- 320
DB 290 YLSHFEEYEDY---ASLKEYPDQSPVLQRFESLQHDCEVLPSPRSNSDQPSLSSQ 346
QY 321 --GOGTENDGFRRTIENGHSRNDVYSEYLNK-----LNL 354
DB 347 GLQMGVLESWSFSSPETPDENDRSYQAKLQDEASTAFGLFAKQTKRPPRONEATNR 406
QY 355 EEPSPVPKCPSLTKRSRAQEOVPOAMTAG-----TSSDMAOPQTPETST-FRNO 407
DB 407 EEEKRRVSHDPFAQQRAR---ENIKSAGARGSDSTSRGLAVQQLSMPATQTVNNNG 463
QY 408 MSPSTGTGPPSPGRNGAEROGNMNSCTPEPN-----PYTGRLVN-----LY 453
DB 464 LYNQGFETGTGTYPPPNLSQMTSTKTPVPETNIPGSTPTMPTFSGPVADDLKTTIF 523
QY 454 KSGYQVGDNNYITMOTTTALPTWGLAPSGKRGLOHPPPVSGQEGKDEPANSRPOGY 513
DB 524 NSSGIQGNHNYMDV-----GLNSQPPNNTCK---EESTSRQQAIF 561
QY 514 NRS 516
DB 562 DNT 564

Search completed: August 13, 2002, 22:08:16
Job time: 3218 sec


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PR 06-AUG-1998; 98US-0095587.
PR 06-AUG-1998; 98US-0095590.
PR 08-SEP-1998; 98US-0099486.
XX
PA (RIGEL-) RIGEL PHARM INC.
PI
PI Luo Y, Huang BCB, Shen M, Yu PW;
XX WPI: 2000-205547/18.
XX
XX Novel apoptotic proteins Apopt1, Apopt2 and Apopt3 and recombinant nucleic
PT acids encoding them for use in screening modulators which is useful for
PT diagnosis and treatment of diseases
XX
PS Claim 1; Fig 6; 64pp: English.
XX
XX The patent discloses the use of novel apoptotic proteins and related
CC molecules involved in apoptosis modulation. Expression vectors
CC comprising the Apopt DNA can be used to transform host cells. Apopt DNA
CC can be administered as DNA vaccines. Apopt proteins are used to make
CC polyclonal and monoclonal antibodies for use in immunotherapy. The
CC proteins are useful in treating apoptosis-mediated disorders including
CC cancer, autoimmune disorders, sustained viral infection, inappropriate
CC cell loss and degenerative disorders. Drug candidates that affect Apopt
CC bioactivity are identified by screening. The present sequence is
CC Apopt3 protein also known as RIP3. This was identified using RIP(receptor
CC interacting protein) as the bait protein employing the yeast two-hybrid
CC screening system. Human Apopt3 is expressed in heart, liver, pancreas,
CC placenta, and lung. This is associated with the TNFalpha (tumour
CC necrosis factor) signalling complex and TNF induced NF (nuclear factor)
CC kappaB transcription factor activation. Overexpression of Apopt3 inhibits
CC TNFalpha-induced caspase activation.
XX
XX Sequence 519 AA:
SO
Query Match 100.0%; Score 2774; DB 21; Length 519;
Best Local Similarity 100.0%; Pred. No. 2.8e-208;
Matches 519; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 MSCVKLPSGAPAPLVISIELENOELVGRDGFVFAORHMKVGYDAVAVTKVSKATSRB 60
DB 1 mscvklpsgapaplviseelengeivgrdgvftrqghkwgydvaavtkvskatsre 60
QY 61 VKAMASLONFVFLRLEGVIEKVMODPKPALVTKFMENGLSGILQSGCPRPPLICRL 120
DB 61 vkamaslonfvflrlegviekvmmodpkpalvtkfmennglsgilsgqcprrppllcrl 120
QY 121 LKEVYLGHFYLDONPYLHRLDKP9NVLPDELHVKLADFGSLTFGGSGSGSGEPE 180
DB 121 lkevylghfyldonpylhrldkpsnvlpdelhvkldfglstfgsgsgsgtsgsep 180
QY 181 GTLGYLAPLFLVNNRKASTADVYSFGLAMAVLAGREVELPTEPSLYEAVCNRNQNP 240
DB 181 gtlgylaplflvnnrkastadvysfgllamavlagrevelptepslyeavcnrnnp 240
QY 241 SLAELPAGETGTLGLKELMOLCKSSPRKRPSPFOCLTKRTDEVQMPENKMAAVST 300
DB 241 slaelpagetgtlglkelmolckssprkrpsfocltkrtdevqmpenmmaavst 300
QY 301 VKDFLSQKSNRFRSIPSSGCGTEMDGFRITENQHSRNDVYSEMLKLNLEPPSS 360
DB 301 vkdfllsqksnrfrsipsogcgtemdgfritenqhsrndvysemllnleppss 360
QY 361 VPKKCPSTRTSRROEOPOAVTACTSDMAOPORPRTSTRRNMBSPSTGTPSPG 420
DB 361 vpkcpsttrtsrroeoavtactsdmaoporprrsttrrnmbpsptgtpspg 420
QY 421 PRGNQGAERQGNMNSCRTEPNPVTGRPLVNIYNC9VQVQDNNYLTMOQTALPTWGLA 480
DB 421 prgnqgaerqgnmnsctepnpvtgrplvniyncs9vqvqdnnylmtqctalptwgl 480
QY 481 PSNGKRGLOHPPPVGSQEGPKDPEAMSRPGQVYHNSGRZ 519

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DB 481 psngkrglohppvgsqegpkdpeamsrpgqvynshgrz 519
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
RESULT 2
AA145046
ID AA145046 standard; Protein: 519 AA.
XX
XX AA145046;
AC
XX
XX 31-MAY-2000 (first entry)
DT
XX
XX Human Apopt3 (K50D) mutant.
DE
XX
XX Apopt3 truncation mutant; Apopt3 protein; apoptotic protein; cytostatic;
KW Immunotherapy; RIP3; receptor-interacting protein; apoptosis modulation;
KW apoptosis-mediated disorder; TNFalpha-induced caspase activation;
KW cancer; autoimmune disorder; cytostatic; degenerative disorder;
KW viral infection; cell loss; inhibitor of apoptosis protein; IAP;
KW TNFalpha signalling complex; tumour necrosis factor.
XX
XX Homo sapiens.
OS
XX
XX Key location/Qualifiers
PH MISC-difference 50 /note- "Wild type Lys is substituted by Asp"
FT
FT MO200007545-A2.
XX
XX 17-FEB-2000.
XX
XX 06-AUG-1999; 99MO-US17776.
XX
XX 06-AUG-1998; 98US-0095587.
XX 06-AUG-1998; 98US-0095590.
XX 08-SEP-1998; 98US-0099486.
XX
XX (RIGEL-) RIGEL PHARM INC.
XX
XX Luo Y, Huang BCB, Shen M, Yu PW;
XX
XX WPI: 2000-205547/18.
XX
XX Novel apoptotic proteins Apopt1, Apopt2 and Apopt3 and recombinant nucleic
PT acids encoding them for use in screening modulators which is useful for
PT diagnosis and treatment of diseases
XX
XX Example 2; Page: 64pp: English.
XX
XX The patent discloses the use of novel apoptotic proteins and related
CC molecules involved in apoptosis modulation. Expression vectors
CC comprising the Apopt DNA can be used to transform host cells. Apopt DNA
CC can be administered as DNA vaccines. Apopt proteins are used to make
CC polyclonal and monoclonal antibodies for use in immunotherapy. The
CC proteins are useful in treating apoptosis-mediated disorders including
CC cancer, autoimmune disorders, sustained viral infection, inappropriate
CC cell loss and degenerative disorders. Drug candidates that affect Apopt
CC bioactivity are identified by screening. The present sequence is a
CC K50D mutant of Apopt3 protein also known as RIP3 (receptor-interacting
CC protein). This was used to demonstrate Apopt3 kinase activity and the
CC activation of cellular caspases by Apopt3. The Apopt3 K50D mutant lost the
CC kinase activity but was still able to activate the caspase activity
CC suggesting that Apopt3's kinase activity is not required for caspase
CC activation and cell death.
CC Note: The present sequence is not given in the specification but is
CC derived from Apopt3 protein (AA145046).
XX
XX Sequence 519 AA:
SO
Query Match 99.8%; Score 2768; DB 21; Length 519;
Best Local Similarity 99.8%; Pred. No. 8.1e-208;
Matches 518; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 1 MSCVKLMPSCAPAPLVSIIELENDLVCKDGFSTVFRAQHRKMGYDAVKIVNSKAISRE 60
DB 1 mscvklmpsgapaplvsiieeleenqelvkgdfstvfraqhrkmgvdaavkivnskaistre 60
QY 61 VKAMASIDNEFVLRLEGVYERVMNDQPKRALYTKRMENKSLGSLQSQCPRPPLICRL 120
DB 61 vkamasidnefvlrllegvylekvmndqpkralytkrmenslsqllsqscprppllcrl 120
QY 121 LKEVVLGMFTLNDQNPVLLHRDLKPSNVLPDELVKRLADFGSLTFQSGSGSGSGEPG 180
DB 121 lkevvlgmftlndqnpvllhrdlkpsnvlpdelhvkrladfgsltfqsgsgsgsgsep 180
QY 181 GTTGVLAPLFLFVNVRKASTADSVYSGILMMAVIAGREVELPTESPVLVEAVCNKRNRP 240
DB 181 gttgvlapflflfvnvrkastadsvysfgilmmavlagrevelptespvlveavcnrnp 240
QY 241 SLAEELPQAGPEPTFGLEGLKELMQLCWSSEPRDRSPQECLEPKTDEYFQVNEENNAVST 300
DB 241 slaelpqagpeptfgleglkelmqcwsseprdrspqeclepktdyfvnenmmaavst 300
QY 301 VKDFLSQLKSSNRRESIPESGCGTEMDGFRTIENQHSNDVMSVEMLNKLNLEPPSS 360
DB 301 vkdfllsqllksnrresfipesgsgtcmdgfrttienghsndvmvsewlnklnleppss 360
QY 361 VPKKCPSLTKRSRAQEDQVPAWTAAGTSSDSMAOPQPTPTSTFRNOMSPSTGTPSPG 420
DB 361 vpkkcpsltkrsraqeqvpawtacgtsdsmaopqptptstfrnompststgtpspg 420
QY 421 PRGQGAERQGMNSCRTPRPVPTGRPLVNIYNCSGVOYGDNNYLTMOOTLALPTWGIA 480
DB 421 prnggaerqgmnsctrpvpvtgrplvniyncsgvdygdnnyltmqotlalptwgla 480
QY 481 PSCKGRGLQHPRPVSGQEGPKDPEAMSRPOGMVNHSGK 518
DB 481 psckgrglqhprrpvsgqegpkdpeawsrpgqvmnhsgk 518

RESULT 3
AAB01524
ID AAB01524 standard; Protein: 518 AA.
XX
AC AAB01524;
XX
DB 08-NOV-2000 (first entry)
XX
DE Kinase of death (KOD).
XX
KW KOD: kinase of death; programmed cell death; apoptosis; cancer;
KW autoimmune disease; stroke; Alzheimer's disease; identification.
XX
OS Homo sapiens.
XX
PN US6096339-A.
XX
PD 01-AUG-2000.
XX
PF 10-JUN-1999; 99US-0329418.
XX
PR 10-JUN-1999; 99US-0329418.
XX
PA (GENE) ZENECA LTD.
XX
PI Gomes BC, Prosser JC, Kasof GM;
XX
XX MPI: 2000-523872/47.
XX
DR N-PSDB: AAA47701, AAA47702.
XX
XX New nucleic acids encoding a protein activator of apoptosis for
XX preventing, diagnosing and treating pathophysiological disorders
XX related to apoptosis
PS Claim 1; Columns 33-36; 32pp; English.

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XX The kinase of death (KOD) polypeptide is integral to the activation
CC process of cellular apoptosis (programmed cell death). Apoptosis is
CC needed to orchestrate biological maintenance of an organism during
CC development as well as to preserve the normal function and fitness of
CC tissues during a normal life span. Physiological conditions which
CC result from aberrant apoptosis may be dire. Cancer and autoimmune
CC disease may result when there is too little apoptosis as well as
CC severe stroke damage or the neurodegeneration of Alzheimer's disease
CC when there is too much apoptosis. The KOD polypeptide is useful for
CC studying pathophysiological disorders related to apoptosis as well
CC as for identifying compounds that modulate biological and/or
CC pharmacological activity of the native mediator of apoptosis.
XX
SQ Sequence 518 AA:
Query Match 99.1%; Score 2750; DB 21; Length 518;
Best Local Similarity 99.4%; Pred. No. 2,1e-206;
Matches 515; Conservative 1; Mismatches 2; Indels 0; Gaps 0:
QY 1 MSCVKLMPSCAPAPLVSIIELENDLVCKDGFSTVFRAQHRKMGYDAVKIVNSKAISRE 60
DB 1 mscvklmpsgapaplvsiieeleenqelvkgdfstvfraqhrkmgvdaavkivnskaistre 60
QY 61 VKAMASIDNEFVLRLEGVYERVMNDQPKRALYTKRMENKSLGSLQSQCPRPPLICRL 120
DB 61 vkamasidnefvlrllegvylekvmndqpkralytkrmenslsqllsqscprppllcrl 120
QY 121 LKEVVLGMFTLNDQNPVLLHRDLKPSNVLPDELVKRLADFGSLTFQSGSGSGSGEPG 180
DB 121 lkevvlgmftlndqnpvllhrdlkpsnvlpdelhvkrladfgsltfqsgsgsgsgsep 180
QY 181 GTTGVLAPLFLFVNVRKASTADSVYSGILMMAVIAGREVELPTESPVLVEAVCNKRNRP 240
DB 181 gttgvlapflflfvnvrkastadsvysfgilmmavlagrevelptespvlveavcnrnp 240
QY 241 SLAEELPQAGPEPTFGLEGLKELMQLCWSSEPRDRSPQECLEPKTDEYFQVNEENNAVST 300
DB 241 slaelpqagpeptfgleglkelmqcwsseprdrspqeclepktdyfvnenmmaavst 300
QY 301 VKDFLSQLKSSNRRESIPESGCGTEMDGFRTIENQHSNDVMSVEMLNKLNLEPPSS 360
DB 301 vkdfllsqllksnrresfipesgsgtcmdgfrttienghsndvmvsewlnklnleppss 360
QY 361 VPKKCPSLTKRSRAQEDQVPAWTAAGTSSDSMAOPQPTPTSTFRNOMSPSTGTPSPG 420
DB 361 vpkkcpsltkrsraqeqvpawtacgtsdsmaopqptptstfrnompststgtpspg 420
QY 421 PRGQGAERQGMNSCRTPRPVPTGRPLVNIYNCSGVOYGDNNYLTMOOTLALPTWGIA 480
DB 421 prnggaerqgmnsctrpvpvtgrplvniyncsgvdygdnnyltmqotlalptwgla 480
QY 481 PSCKGRGLQHPRPVSGQEGPKDPEAMSRPOGMVNHSGK 518
DB 481 psckgrglqhprrpvsgqegpkdpeawsrpgqvmnhsgk 518

RESULT 4
AAB09430
ID AAB09430 standard; Protein: 518 AA.
XX
AC AAB09430;
XX
DB 19-NOV-2001 (first entry)
XX
DE Human kinase of death (KOD) protein activator of apoptosis.
XX
KW Human; protein activator; apoptosis; kinase of death; KOD; therapy;
KW cytostatic.
XX
OS Homo sapiens.
XX

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Key Location/Qualifiers
 Domain 21..281
 /note= "kinase domain"
 Misc-difference 83..85
 /note= "Encoded by GCGGCGTCGAGC; This occurs while decoding with AAD16312"
 Misc-difference 112
 /note= "Encoded by YGG; This occurs while decoding with AAD16313"
 Domain 280..518
 /note= "Death domain"
 US6267956-B1.
 31-JUL-2001.
 21-MAR-2000; 2000DS-0531914.
 10-JUN-1999; 99US-0329418.
 (ZENE) ZENECA LTD.
 Gomes BC, Kasof GM, Prosser JC;
 WPI; 2001-535022/59.
 N-PSDB; AAD16312, AAD16313.
 New human protein activator protein, useful for treating dysfunctional apoptosis conditions and in screening assays to identify agonists which agonize or mimic biological and/or pharmacological activity -
 Claim 1; Column 33-36; 31pp; English.
 The invention relates to human protein activator of apoptosis and methods to identify compounds that modulate the biological and/or pharmacological activity of the activator and hence regulate apoptosis. The nucleic acid and amino acid sequences of the kinase of death (KOD) are useful for identifying compounds that modulate the biological and/or pharmacological activity of a native mediator of apoptosis, for treating dysfunctional apoptosis conditions, in screening assays to identify agonists which agonize or mimic biological and/or pharmacological activity, induce production of or prolong the biological half-life of the molecule in vivo or in vitro. The present sequence is human KOD protein activator of apoptosis.
 Sequence 518 AA:

Query Match 99.18; Score 2750; DB 22; Length 518;
 Best Local Similarity 99.48; Pred. No. 2.1e-206;
 Matches 515; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MSCVCLMPGAPAPLVSIELENOELVGKDGCTVFRQAQHRKMGYDAVKIVNSKASISRE 60
 DB 1 mscvclmpgapepivsleelengelyvgfgtvtfaqrkwydvavkivnsalare 60
 QY 61 VYAKASLDNEFVLRLGEGYEKVMNDOPKRALVTKFMENSGSLGQSCPPFNLRL 120
 DB 61 vkamasldnefvlrllegylekvmndopkralvtkfmengslsgllqscppfnpfllrcl 120
 QY 121 LKEVYLGAFYLDONPVILHRDLKPSNVLPDPELHVKLADFGISTFGSGSGSTSGERG 180
 DB 121 lkevylgafyldonpvlilhrdlkpsnvlpdpeelhvkkladfgistfgsgsgstsgerg 180
 QY 181 GTGLYLABELFVNNVRKASTADYVSGIIMAVLAGREVELPTPEPSLVYEAVCRRQRRP 240
 DB 181 gtglylabelfvnnvrkastadyvsgiiimavlagrevelptpepslvyeavcrrqrrp 240
 QY 241 SLAEIPGAGPEPTGEGKELMOLCWSSEPKDRSPFOECLPTDREYQVNNMAAYST 300
 DB 241 slaelpgagpetglegkelmolcwssepkdrspfoeclptdreymnmaayst 300
 QY 301 VADFLSQAKSNRRFSIPESGGGTGKDFRRTIENQHSNDVNVSEWLKLNLEPPSS 360
 DB 301 vadflsqaksnrrfsipesgggtgkdfrrtiennqhsndvnnsewlklnleppss 360

DB 301 vkdfllsqaksnrrfsipesgggtgkdfrrtiennqhsndvnnsewlklnleppss 360
 QY 361 VPKKPSLTKRSRAOEDVPOAMTACTSBSMAOPPOPTETSTFRNQPSPRTSGTSPG 420
 DB 361 vpkkpsltkrsraqeeyvpqavtaglsdsmaqppqtpeltsifnqmpspclsgtspg 420
 QY 421 PRGNQAGRGGMNMSCRTPPEPNPTGRPLVINYNCSGVGVGNMTLTMOQTALPTWGLA 480
 DB 421 prngnagrggmnmwscrtpppnptgrplvinyncsgvvgvgnmlyltmqgtalptwgl 480
 QY 481 PSGKRGCLDHPPEVGSQSGFKDPAKSRPQGTNRHSGK 518
 DB 481 psgkrgcldhppvgsqsgfkdpaksrpqgtnrhsgk 518
 RESULT 5
 AAB01526
 ID AAB01526 standard; Protein: 518 AA.
 AC AAB01526;
 DT 08-NOV-2000 (first entry)
 DX Kinase of death (KOD) dominant negative mutant.
 DE KOD; kinase of death; programmed cell death; apoptosis; cancer; autoimmune disease; stroke; Alzheimer's disease; identification.
 KW Homo sapiens.
 OS
 XX US6096539-A.
 PM 01-AUG-2000.
 PD 10-JUN-1999; 99US-0329418.
 PF 10-JUN-1999; 99US-0329418.
 PR 10-JUN-1999; 99US-0329418.
 XX (ZENE) ZENECA LTD.
 PA Gomes BC, Prosser JC, Kasof GM;
 PI WPI; 2000-523872/47.
 DR New nucleic acids encoding a protein activator of apoptosis for preventing, diagnosing and treating pathophysiological disorders related to apoptosis
 PT
 PT
 PT
 PS Claim 5; Columns 37-40; 32pp; English.
 The kinase of death (KOD) polypeptide is integral to the activation process of cellular apoptosis (programmed cell death). Apoptosis is needed to orchestrate biological maintenance of an organism during development as well as to preserve the normal function and fitness of tissues during a normal life span. Physiological conditions which result from aberrant apoptosis may be dire. Cancer and autoimmune disease may result when there is too little apoptosis as well as severe stroke damage or the neurodegeneration of Alzheimer's disease when there is too much apoptosis. The KOD polypeptide is useful for studying pathophysiological disorders related to apoptosis as well as for identifying compounds that modulate biological and/or pharmacological activity of the native mediator of apoptosis. This KOD dominant negative mutant sequence differs from the wild type KOD (AAB01524) by having lysine at position 50 (ATP binding site) replaced by arginine.

Sequence 518 AA:

Query Match 99.08; Score 2747; DB 21; Length 518;
 Best Local Similarity 99.28; Pred. No. 3.5e-206;
 Matches 514; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

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OY 1 MSCVKLMPGAPAPLVISELENOELVGRDGFVFRQHRKMGYDAVKIYNSKAISRE 60
    |||
DB 1 mscklvpsgapaplviselelenqelvgkgfgrqhkwydvavilvnskaistre 60
OY 61 VKAMASLDNEFVLEGVIEKVMODDPKALVTFEMNGSLGLOSOCPRPMLICRL 120
    |||
DB 61 vkamaldnefvlegviekvmddpkaalvtkfmgngslgllsqgcprrpmllicrl 120
OY 121 LKEVYLGMFYLDQNPVYLHRDLKPSNVLPDELVKTLADFGLSFGGSGSGSGSGEPG 180
    |||
DB 121 lkevylgmfyldqnpvylhrdlkpsnvllpdelvkladfglsftfgsgsgsgsgsep 180
OY 181 GTLGVLAPELFVYNNRKAASADVTSFGILMMAYLAGREVELPTPEGLSYEAACNRRNP 240
    |||
DB 181 gtlgvlapelvfynnrkaasadvtsfgilmmavlagrevelptepglsyeaacnrrnp 240
OY 241 SLAELPQAGPPTGEGIEKLMQLCWSSEPKRPSFOCLKRTDEVQVYENNNMAAVST 300
    |||
DB 241 slaelpqagpptegeiekmlqlcwssepkdrpsfoclkrtdeviqvymnmaavst 300
OY 301 VKDELSQLKSSNNRRFSIPESGOGCTEMDGFRTIENQHSRNDVYSEMLKLNLEPPSS 360
    |||
DB 301 vkdelsqlkssnnrrfsipesgogctemdgrftriensrndvymsemlklnleppss 360
OY 361 VPKKCPSLTKRSRAOEVOYPAWTAGTSSDMAOPPOPTSTFRNQMPSPTSTGTPSPG 420
    |||
DB 361 vpkkcpsltkrsraoevoypawtagtssdmasppopptstfrnqmppsptstgtpspg 420
OY 421 PRGNQGAEROGMNMNSCRTPENPVGTGRPLVNTNCSGVQVGDNNYLTMOQTALPTWGLA 480
    |||
DB 421 prngngaerogmnmnsctrepnpvtgrplvntncsgvqvgdnnyltmqotalptwgl 480
OY 481 PSKGRGLQHPPIPVGSOEGPKDEPANSRPOGWYNHSGK 518
    |||
DB 481 pskgrglqhppipvgsoegpkdepaansrpqwyynhsgk 518

RESULT 6
AAE09432
ID AAE09432 standard; Protein: 518 AA.
AC AAE09432;
XX
DT 19-NOV-2001 (first entry)
XX
DE Human kinase of death (KOD) dominant negative mutant, K50R.
XX
KW Human; protein activator; apoptosis; kinase of death; KOD; therapy;
KW cytosolic; mutant; muten.
XX
OS Homo sapiens.
XX
OS Synthetic.
XX
PN US6267956-B1.
XX
PD 31-JUL-2001.
XX
PF 21-MAR-2000; 2000US-0531914.
XX
PR 10-JUN-1999; 99US-0329418.
XX
PA (ZENEC) ZENECA LTD.
XX
PI Gomes BC, Kasof GM, Prosser JC;
XX
DR WPI; 2001-535022/59.
XX
PT New human protein activator protein, useful for treating dysfunctional
PT apoptosis conditions and in screening assays to identify agonists which
PT agonize or mimic biological and/or pharmacological activity -
XX
XX Disclosure: Column 37-40; 31pp; English.

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XX The invention relates to human protein activator of apoptosis and
CC methods to identify compounds that modulate the biological and/or
CC pharmacological activity of the activator and hence regulate
CC apoptosis. The nucleic acid and amino acid sequences of the kinase
CC of death (KOD) are useful for identifying compounds that modulate
CC the biological and/or pharmacological activity of a native mediator
CC of apoptosis, for treating dysfunctional apoptosis conditions, in
CC screening assays to identify agonists which agonize or mimic
CC biological and/or pharmacological activity, induce production of or
CC prolong the biological half-life of the molecule in vivo or in vitro.
CC The present sequence is a dominant negative mutant of human KOD
CC protein activator of apoptosis. The lysine at position 50 of native
CC KOD is changed to arginine in the mutant sequence.
XX
SQ Sequence 518 AA:

Query Match 99.0%; Score 2747; DB 22; Length 518;
Best Local Similarity 99.2%; Pred. No. 3,5e-206;
Matches 514; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 1 MSCVKLMPGAPAPLVISELENOELVGRDGFVFRQHRKMGYDAVKIYNSKAISRE 60
    |||
DB 1 mscklvpsgapaplviselelenqelvgkgfgrqhkwydvavilvnskaistre 60
OY 61 VKAMASLDNEFVLEGVIEKVMODDPKALVTFEMNGSLGLOSOCPRPMLICRL 120
    |||
DB 61 vkamaldnefvlegviekvmddpkaalvtkfmgngslgllsqgcprrpmllicrl 120
OY 121 LKEVYLGMFYLDQNPVYLHRDLKPSNVLPDELVKTLADFGLSFGGSGSGSGSGEPG 180
    |||
DB 121 lkevylgmfyldqnpvylhrdlkpsnvllpdelvkladfglsftfgsgsgsgsgsep 180
OY 181 GTLGVLAPELFVYNNRKAASADVTSFGILMMAYLAGREVELPTPEGLSYEAACNRRNP 240
    |||
DB 181 gtlgvlapelvfynnrkaasadvtsfgilmmavlagrevelptepglsyeaacnrrnp 240
OY 241 SLAELPQAGPPTGEGIEKLMQLCWSSEPKRPSFOCLKRTDEVQVYENNNMAAVST 300
    |||
DB 241 slaelpqagpptegeiekmlqlcwssepkdrpsfoclkrtdeviqvymnmaavst 300
OY 301 VKDELSQLKSSNNRRFSIPESGOGCTEMDGFRTIENQHSRNDVYSEMLKLNLEPPSS 360
    |||
DB 301 vkdelsqlkssnnrrfsipesgogctemdgrftriensrndvymsemlklnleppss 360
OY 361 VPKKCPSLTKRSRAOEVOYPAWTAGTSSDMAOPPOPTSTFRNQMPSPTSTGTPSPG 420
    |||
DB 361 vpkkcpsltkrsraoevoypawtagtssdmasppopptstfrnqmppsptstgtpspg 420
OY 421 PRGNQGAEROGMNMNSCRTPENPVGTGRPLVNTNCSGVQVGDNNYLTMOQTALPTWGLA 480
    |||
DB 421 prngngaerogmnmnsctrepnpvtgrplvntncsgvqvgdnnyltmqotalptwgl 480
OY 481 PSKGRGLQHPPIPVGSOEGPKDEPANSRPOGWYNHSGK 518
    |||
DB 481 pskgrglqhppipvgsoegpkdepaansrpqwyynhsgk 518

RESULT 7
AAE01525
ID AAE01525 standard; Protein: 518 AA.
AC AAE01525;
XX
DT 08-NOV-2000 (first entry)
XX
DE Kinase of death (KOD) dominant negative mutant.
XX
KW KOD; kinase of death; programmed cell death; apoptosis; cancer;
KW autoimmune disease; stroke; Alzheimer's disease; identification.
XX
XX Homo sapiens.

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XX US6096539-A.
 PN 01-ANG-2000.
 XX 10-JUN-1999; 9905-0329418.
 XX 10-JUN-1999; 9905-0329418.
 XX (ZENEC) ZENEC LTD.
 PI Gomes BC, Prosser JC, Kasof GM;
 DR WPI; 2000-523872/47.
 XX New nucleic acids encoding a protein activator of apoptosis for
 PT preventing, diagnosing and treating pathophysiological disorders
 PT related to apoptosis
 XX
 PS Claim 5; Columns 35-38; 32pp; English.
 XX The kinase of death (KOD) polypeptide is integral to the activation
 CC process of cellular apoptosis (programmed cell death). Apoptosis is
 CC needed to orchestrate biological maintenance of an organism during
 CC development as well as to preserve the normal function and fitness of
 CC tissues during a normal life span. Physiological conditions which
 CC result from aberrant apoptosis may be dire. Cancer and autoimmune
 CC disease may result when there is too little apoptosis as well as
 CC severe stroke damage or the neurodegeneration of Alzheimer's disease
 CC when there is too much apoptosis. The KOD polypeptide is useful for
 CC studying pathophysiological disorders related to apoptosis as well
 CC as for identifying compounds that modulate biological and/or
 CC pharmacological activity of the native mediator of apoptosis.
 CC This KOD dominant negative mutant sequence differs from the wild
 CC type KOD (AAB01524) by having alanine at position 142 instead of
 CC aspartic acid.
 CC
 SO Sequence 518 AA;
 Query Match 98.8%; Score 2742; DB 21; Length 518;
 Best Local Similarity 99.2%; Pred. No. 8.7e-206;
 Matches 514; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

DB 421 prngnsgaergmmscrtpenpvtgrplvnlncsgvqgdanlyltmgqtaipwja 480
 QY 481 psgkrgclqhprrpygsoeqekpdpnansrpoctwnhsrk 518
 DB 481 psgkrgclqhprrpygsoeqekpdpnansrpoctwnhsrk 518
 RESULT 8
 AAE09431
 ID AAE09431 standard; Protein; 518 AA.
 AC AAE09431;
 DT 19-NOV-2001 (first entry)
 XX Human kinase of death (KOD) dominant negative mutant, D143A.
 DE Human kinase of death (KOD) dominant negative mutant, D143A.
 XX
 KW Human; protein activator; apoptosis; kinase of death; KOD; therapy;
 KW cyclostatic; mutant; mutain.
 XX Homo sapiens.
 OS Synthetic.
 XX US6267956-B1.
 XX 31-JUL-2001.
 XX
 PF 21-MAR-2000; 2000US-0531914.
 XX 10-JUN-1999; 9905-0329418.
 XX (ZENEC) ZENEC LTD.
 PI Gomes BC, Kasof GM, Prosser JC;
 DR WPI; 2001-535022/59.
 XX New human protein activator protein, useful for treating dysfunctional
 PT apoptosis conditions and in screening assays to identify agonists which
 PT agonize or mimic biological and/or pharmacological activity -
 XX
 PS Example 8; Column 35-38; 31pp; English.
 XX The invention relates to human protein activator of apoptosis and
 CC methods to identify compounds that modulate the biological and/or
 CC pharmacological activity of the activator and hence regulate
 CC apoptosis. The nucleic acid and amino acid sequences of the kinase
 CC of death (KOD) are useful for identifying compounds that modulate
 CC the biological and/or pharmacological activity of a native mediator
 CC of apoptosis, for treating dysfunctional apoptosis conditions, in
 CC screening assays to identify agonists which agonize or mimic
 CC biological and/or pharmacological activity, induce production of or
 CC prolong the biological half-life of the molecule in vivo or in vitro.
 CC The present sequence is a dominant negative mutant of human KOD
 CC protein activator of apoptosis. The aspartic acid at position 143
 CC of native KOD is changed to alanine in the mutant sequence.
 CC Note: Column 11 of this specification describes that mutation occurs
 CC at position Asp143 of native KOD. But Asp is at position 142 in the
 CC native KOD sequence shown in sequence listing.
 CC
 SO Sequence 518 AA;
 Query Match 98.8%; Score 2742; DB 22; Length 518;
 Best Local Similarity 99.2%; Pred. No. 8.7e-206;
 Matches 514; Conservative 1; Mismatches 3; Indels 0; Gaps 0;


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Db 61 VKAMASLDNEFVLRSGVLEKWNQDQPKPALVCKFMENSLGSLIGSQCPRPVPLLCRL 120
QY 121 LKEVYLGMEFLHDONPYLLHRDLKPSNTVLPPELHVKLADFGSLTFQSGSGSGSGERG 180
Db 121 LKEVYLGMEFLHDONPYLLHRDLKPSNTVLPPELHVKLADFGSLTFQSGSGSGSGERG 180
QY 181 GTLGYLAPELFVNVRKASTASDVYSFGILMAYLAGREVELPTEPSLYEAVCNQNRP 240
Db 181 GTLGYLAPELFVNVRKASTASDVYSFGILMAYLAGREVELPTEPSLYEAVCNQNRP 240
QY 241 SLAELPQAGPEPTGLGELKELMQLCMSSEPRDRPSFOCLPKTDEVFQVNNMNAAVST 300
Db 241 SLAELPQAGPEPTGLGELKELMQLCMSSEPRDRPSFOCLPKTDEVFQVNNMNAAVST 300
QY 301 VKDFLSQKSSNRFSIPESGGGTENQGFRTIENQSRNDVYVSEMLNKLMLPEPPS 360
Db 301 VKDFLSQKSSNRFSIPESGGGTENQGFRTIENQSRNDVYVSEMLNKLMLPEPPS 360
QY 361 VPKKCPSLTRKRAQEDQYPOAWTAGTSSDMAOPPTPTSTRNOMSPSTGTSPSG 420
Db 361 VPKKCPSLTRKRAQEDQYPOAWTAGTSSDMAOPPTPTSTRNOMSPSTGTSPSG 420
QY 421 PRGNQGAERGMNMSCRTPEPNVGRPLVNIYNCSGVOVDNNYLTMOQTALPTMGIA 480
Db 421 PRGNQGAERGMNMSCRTPEPNVGRPLVNIYNCSGVOVDNNYLTMOQTALPTMGIA 480
QY 481 PSGKRGILQHPVPVGSQEGPKDPEASRPQGWYHNSGK 518
Db 481 PSGKRGILQHPVPVGSQEGPKDPEASRPQGWYHNSGK 518

RESULT 9
AAB01530 standard; Protein: 518 AA.
ID AAB01530:
AC AAB01530:
XX 08-NOV-2000 (first entry)
XX 08-NOV-2000 (first entry)
DE Kinase of death (KOD) dominant negative mutant.
XX Kinase of death (KOD) dominant negative mutant.
XX KOD; kinase of death; programmed cell death; apoptosis; cancer;
XX autoimmune disease; stroke; Alzheimer's disease; identification.
XX Homo sapiens.
XX US6096539-A.
XX US6096539-A.
XX 01-AUG-2000.
XX 01-AUG-2000.
XX 10-JUN-1999; 9905-0329418.
XX 10-JUN-1999; 9905-0329418.
XX 10-JUN-1999; 9905-0329418.
XX (ZENNE) ZENNECA LTD.
XX (ZENNE) ZENNECA LTD.
XX Gomes BC, Prosser JC, Kasof GM;
XX WPI; 2000-523872/47.
XX WPI; 2000-523872/47.
XX New nucleic acids encoding a protein activator of apoptosis for
XX preventing, diagnosing and treating pathophysiological disorders
XX related to apoptosis
XX related to apoptosis
XX Clain 5; Columns 45-48; 32pp; English.
XX Clain 5; Columns 45-48; 32pp; English.
XX The kinase of death (KOD) polypeptide is integral to the activation
XX process of cellular apoptosis (programmed cell death). Apoptosis is
XX needed to orchestrate biological maintenance of an organism during
XX development as well as to preserve the normal function and fitness of
XX tissues during a normal life span. Physiological conditions which
XX result from aberrant apoptosis may be dire. Cancer and autoimmune

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CC disease may result when there is too little apoptosis as well as
CC severe stroke damage or the neurodegeneration of Alzheimer's disease
CC when there is too much apoptosis. The KOD polypeptide is useful for
CC studying pathophysiological disorders related to apoptosis as well
CC as for identifying compounds that modulate biological and/or
CC pharmacological activity of the native mediator of apoptosis.
CC This KOD dominant negative mutant sequence differs from the wild
CC type KOD (AAB01524) by having both tryptophan residues at positions
CC 435 and 478 replaced by alanine.
CC XX
SQ Sequence 518 AA:
Query Match 98.1%; Score 2722; DB 21; Length 518;
Best Local Similarity 99.0%; Pred. No. 3,26-204;
Matches 513; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
QY 1 MSCRTLPKSGAPRLVYSIFELFENQELVKGQGTGYFRQAHKTKGYDVAVYVNSKATSE 60
Db 1 MSCRTLPKSGAPRLVYSIFELFENQELVKGQGTGYFRQAHKTKGYDVAVYVNSKATSE 60
QY 61 VKAMASLDNEFVLRSGVLEKWNQDQPKPALVCKFMENSLGSLIGSQCPRPVPLLCRL 120
Db 61 VKAMASLDNEFVLRSGVLEKWNQDQPKPALVCKFMENSLGSLIGSQCPRPVPLLCRL 120
QY 121 LKEVYLGMEFLHDONPYLLHRDLKPSNTVLPPELHVKLADFGSLTFQSGSGSGSGERG 180
Db 121 LKEVYLGMEFLHDONPYLLHRDLKPSNTVLPPELHVKLADFGSLTFQSGSGSGSGERG 180
QY 181 GTLGYLAPELFVNVRKASTASDVYSFGILMAYLAGREVELPTEPSLYEAVCNQNRP 240
Db 181 GTLGYLAPELFVNVRKASTASDVYSFGILMAYLAGREVELPTEPSLYEAVCNQNRP 240
QY 241 SLAELPQAGPEPTGLGELKELMQLCMSSEPRDRPSFOCLPKTDEVFQVNNMNAAVST 300
Db 241 SLAELPQAGPEPTGLGELKELMQLCMSSEPRDRPSFOCLPKTDEVFQVNNMNAAVST 300
QY 301 VKDFLSQKSSNRFSIPESGGGTENQGFRTIENQSRNDVYVSEMLNKLMLPEPPS 360
Db 301 VKDFLSQKSSNRFSIPESGGGTENQGFRTIENQSRNDVYVSEMLNKLMLPEPPS 360
QY 361 VPKKCPSLTRKRAQEDQYPOAWTAGTSSDMAOPPTPTSTRNOMSPSTGTSPSG 420
Db 361 VPKKCPSLTRKRAQEDQYPOAWTAGTSSDMAOPPTPTSTRNOMSPSTGTSPSG 420
QY 421 PRGNQGAERGMNMSCRTPEPNVGRPLVNIYNCSGVOVDNNYLTMOQTALPTMGIA 480
Db 421 PRGNQGAERGMNMSCRTPEPNVGRPLVNIYNCSGVOVDNNYLTMOQTALPTMGIA 480
QY 481 PSGKRGILQHPVPVGSQEGPKDPEASRPQGWYHNSGK 518
Db 481 PSGKRGILQHPVPVGSQEGPKDPEASRPQGWYHNSGK 518

RESULT 10
AAE09436 standard; Protein: 518 AA.
ID AAE09436:
AC AAE09436:
XX 19-NOV-2001 (first entry)
XX 19-NOV-2001 (first entry)
XX Human kinase of death (KOD) dominant negative mutant, W435A/W478A.
XX Human kinase of death (KOD) dominant negative mutant, W435A/W478A.
XX Human; protein activator; apoptosis; kinase of death; KOD; therapy;
XX cytosolic; mutant; mutain.
XX Human; protein activator; apoptosis; kinase of death; KOD; therapy;
XX cytosolic; mutant; mutain.
XX Homo sapiens.
XX Synthetic.
XX US6267956-B1.
XX US6267956-B1.
XX 31-JUL-2001.
XX 31-JUL-2001.

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XX 21-MAR-2000; 2000US-0531914.
 PF 10-JUN-1999; 99US-0329418.
 XX (ZENE) ZENECA LTD.
 XX Gomez BC, Kasof GM, Prosser JC;
 XX WPI: 2001-535022/59.
 DR New human protein activator protein, useful for treating dysfunctional
 PT apoptosis conditions and in screening assays to identify agonists which
 PT agonize or mimic biological and/or pharmacological activity -
 PS Disclosure: Column 45-48; 31pp: English.
 XX The invention relates to human protein activator of apoptosis and
 CC methods to identify compounds that modulate the biological and/or
 CC pharmacological activity of the activator and hence regulate
 CC apoptosis. The nucleic acid and amino acid sequences of the kinase
 CC of death (KOD) are useful for identifying compounds that modulate
 CC the biological and/or pharmacological activity of a native mediator
 CC of apoptosis, for treating dysfunctional apoptosis conditions, in
 CC screening assays to identify agonists which agonize or mimic
 CC biological and/or pharmacological activity, induce production of or
 CC prolong the biological half-life of the molecule in vivo or in vitro.
 CC The present sequence is a dominant negative mutant of human KOD
 CC and 478 of native KOD are changed to alanine in the mutant sequence.
 CC Note: Column 12 of this specification describes that mutation occurs
 CC at positions Trp435 and Trp478 of native KOD. But Trp are at positions
 CC 434 and 477 in the native KOD sequence shown in sequence listing.
 XX
 SQ Sequence 518 AA:
 Query Match 98.1%; Score 2723; DB 22; Length 518;
 Best Local Similarity 99.0%; Pred. No. 3.2e-204;
 Matches 513; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
 QY 1 MSCVRLMPGAPAPLVSTIELENDLVKDDFGTFVPAQRKRGYDAVAVYNSKAISRE 60
 DB 1 mscvrlmpgapaaplvslelelenglvkggfgtvtqqrkrgydvavynskaisre 60
 QY 61 VKAMALDNEPVLRLGEGYEVNMDOPKRALYRKEMNSLSGLQSQCPRPMLLCL 120
 DB 61 vkamaldfeyrllegylvknwdqdkpalkvckfmeingslglqsgcprrpmlcll 120
 QY 121 LKEVYLGKCYLHDQNPVLLHDLKPSNYLPDELHVRLADFGSLTFGGSQSGSGERG 180
 DB 121 lkevylgmfyldhqpvlhhdlkpsnvlldpelnhvkldfgsltfggsgsgsgerg 180
 QY 181 GTLGAYLAPLFPVNNRKAASSTASDVSTFGLMMAVLAGREVELPTESLVEAVCNRNRP 240
 DB 181 gtlgylapelfvnnrkastadvsfsgllmmavlagrevelpteslveyavcnrnrrp 240
 QY 241 SLAELPQAGPEPTGLGKLELMQKCHSEPERDRSPFECPLKTDVFPQVNNMNAAYST 300
 DB 241 slaelpqagpeptglgklemqkchseperdrspfecplktdevfpqvnmmnaayst 300
 QY 301 VDDFTLSQLKSNRRRPSIPESGOGGTENDGFRRTIENHSHNDVAVSEWLNKLLEPPSS 360
 DB 301 vdfdtlsqllsnrrpsipesgoggtendgfrttiennshndvavsewlnklleppss 360
 QY 361 VPKKPSLTKRRRAQEDQVPOAMTACTSSDSMAOPPTPTSTFRNOMSPSTGTPSPG 420
 DB 361 vpkkpsltkrrraqedqvpoamtactssdsmaopptptstfrnomsptstgtpspg 420
 QY 421 PRGNQAGKGNKNSCRPERPPTGRLPVNTYKSGVGVGDNNYLYMQQTALPTMGLA 480
 DB 421 prgnqagkgnknscreperpvtgrlpvntynksgvgvgdnnylmqqtaltptmgl 480
 DB 421 prgnqagkgnknscreperpvtgrlpvntynksgvgvgdnnylmqqtaltptgla 480

QY 481 PSQKRGLOHPPVSGSGEKDPEANSPQGTWNSGR 518
 DB 481 psqkrglqhppvsgsgdkdpeanspqgtwnsgk 518
 RESULT 11
 AAB6604
 ID AAB6604 standard; protein; 497 AA.
 XX
 AC AAB6604;
 XX
 DT 04-APR-2001 (first entry)
 XX
 DE Human h15590 protein.
 XX
 KW Human; protein kinase; cell growth; tumour; cancer; immune;
 KW Inflammatory; respiratory; haematological; bone disorder.
 XX
 OS Homo sapiens.
 XX
 PN W0200100879-A1.
 XX
 PD 04-JAN-2001.
 XX
 PF 30-JUN-2000; 2000MO-US18291.
 XX
 PR 30-JUN-1999; 99US-0345473.
 PR 01-MAY-2000; 2000US-0562480.
 XX
 PA (MILL-) MILLENNIUM PHARM INC.
 XX
 PI Hodge MR, Meyers R, Williamson M;
 DR WPI: 2001-061977/07.
 XX
 PT New protein kinase polypeptides, nucleic acids and anti-kinase
 PT antibodies, useful for diagnosing and treating e.g. cancer,
 PT Inflammatory, immune, cardiovascular and bone disorders -
 PS Claim 1: Fig 10; 93pp: English.
 XX
 CC The present invention relates to human protein kinase. The proteins
 CC are from new human genes termed h12832, h14138, h15990,
 CC h15993, h16541 and h2252. The proteins may be used to identify
 CC modulators of their activity. The proteins may also be used to derive
 CC products for the treatment of cellular growth related disorders,
 CC malignancies, cancers, immune, inflammatory, respiratory,
 CC haematological and bone-related disorders.
 XX
 SQ Sequence 497 AA:
 Query Match 95.1%; Score 2639; DB 22; Length 497;
 Best Local Similarity 99.4%; Pred. No. 9.2e-198;
 Matches 494; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 22 ENDELVKKDGFVTPRAQRKNGIDVAVKYNSTASISREYKAMASLNEPVLRLGEGY 81
 DB 22 endelvkgdgvtpraqrkngidvavkynstasisevkmasslnefvlrlgelyek 81
 QY 82 VNMDDPKPALVYKEMENSLSGLLQSQCPRPMLLCLRLKEVYLGKCYLHDQNPVLLHR 141
 DB 82 vnmddpkpalvlykemensslsgllqsgcprrpmlclrlkevylgmfyldhqpvlhrr 141
 QY 142 DLRKSNVLPDELHVRLADFGSLTFGGSQSGSGERGCTGLYLAPELFPVNNRKAAS 201
 DB 142 dlrsnvlldpelnhvkldfgsltfggsgsgsgergctglylapelfvnnrkasta 201
 QY 201 SDVYSFGILLMMAVLAGREVELPTESLVEAVCNRNRPISLAELPQAGPEPTGLGKLE 261
 DB 201 sdvysfgillmmavlagrevelpteslveyavcnrnripislaelpqagpeptglgk 261
 DB 181 sdvysfgillmmavlagrevelpteslveyavcnrnripislaelpqagpeptglgk 261
 QY 262 MQLCWSSEPRDRSPFECPLKTDVFPQVNNMNAAYSTVKDFLSLSSRRRSIPESG 321

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Db 241 mqlwseppidrpstfegclpkddevfqmvenmmaaavetvdfisqrltrssnrffsipeeg 300
Oy 322 OGGTENDGFRRITENQHSRNDVWSEMLNKLLEPPSSVPKPKCPSLTNKSRAOEQVQ 381
Db 301 gggfemgffrrclenqsrndwvsewlnklnleppsvpkckpsltkrsgaqevpq 360
Oy 382 AWTAGTSSDAMAPQPTPERSFRRNOMPSPTGTPSPGPGNGGARQGNMNSCRTPRP 441
Db 361 awtqgsdamaqpqtptetsfrnqmpscscgcpqpgpqnqgaerqgmavscrtpep 420
Oy 442 NPVTGRPLVNYKCGVQVGDNNYLTMOQTALPTWGLAPSGKRGIGHPVYGSQEGPK 501
Db 421 npvtgrplvnykncsvqyqdmnyltmqqtalptwglapsgkrgigpdpvgsqgdpk 480
Oy 502 DPEAMSRPOGMVNRSGK 518
Db 481 dpeawsrpgvnyhsgk 497

RESULT 12
AAB18658
ID AAB18658 standard; Protein; 485 AA.
XX
AC AAB18658;
XX
DT 22-JAN-2001 (first entry)
XX
DE A human regulator of intracellular phosphorylation.
XX
KW Human; intracellular phosphorylation regulator; HRIP; stroke; myeloma;
KW neurological disorder; Parkinson's disease; demyelinating disease;
KW meningitis; developmental disorder; neuromuscular disorder; cancer;
KW myasthenia gravis; cell proliferative disorder; actinic keratosis;
KW arteriosclerosis; leukemias; melanoma; bronchitis;
KW autoimmune disorder; inflammatory disorder; Addison's disease;
KW acquired immunodeficiency disease; allergy; diabetes mellitus;
KW rheumatoid arthritis; microbial infection; trauma.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Modified-site 16 /note= "potential phosphorylation site"
FT Domain 26..247 /note= "eukaryotic protein kinase domain"
FT Modified-site 66 /note= "potential glycosylation site"
FT Active-site 105..117 /note= "potential phosphorylation site"
FT Modified-site 166 /note= "protein kinase catalytic site"
FT Modified-site 167 /note= "potential phosphorylation site"
FT Modified-site 208 /note= "potential phosphorylation site"
FT Modified-site 242 /note= "potential phosphorylation site"
FT Modified-site 267 /note= "potential phosphorylation site"
FT Modified-site 278 /note= "potential phosphorylation site"
FT Modified-site 283 /note= "potential phosphorylation site"
FT Modified-site 283 /note= "potential phosphorylation site"
FT Modified-site 292 /note= "potential phosphorylation site"
FT Modified-site 306 /note= "potential phosphorylation site"
FT Modified-site 336 /note= "potential phosphorylation site"
FT Modified-site 354 /note= "potential phosphorylation site"

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FT Modified-site 370 /note= "potential phosphorylation site"
FT Modified-site 400 /note= "potential phosphorylation site"
FT Modified-site 402 /note= "potential glycosylation site"
FT Modified-site 412 /note= "potential phosphorylation site"
FT Modified-site 421 /note= "potential phosphorylation site"
FT Modified-site 449 /note= "potential glycosylation site"
FT Modified-site 481 /note= "potential phosphorylation site"
FT Modified-site 483 /note= "potential glycosylation site"
FT Modified-site 483 /note= "potential phosphorylation site"
PN W0200055332-A2.
PD 21-SEP-2000.
PE 17-MAR-2000; 2000MO-DS07277.
PX 18-MAR-1999; 99US-0125593.
PR 20-MAY-1999; 99US-0135049.
PR 09-JUL-1999; 99US-0143188.
PX (INCY-) INCYTE PHARM INC.
PI Bandman O, Tang YT, Yue H, Hillman JT, Baughn MR, Azimzai Y;
PI Lu DM, Au-Young J;
PX WPI: 2000-602121/57.
DR N-PSDB; AAA75675.
XX Novel human intracellular phosphorylation regulator polypeptides and
PT polynucleotides for diagnosis, prevention and treatment of
PT neurological, cell proliferative and autoimmune/inflammatory disorders
PT -
PX Claim 1: Page 76-77; 96pp; English.
XX
CC The present sequence represents a human regulator of intracellular
CC phosphorylation (HRIP). HRIP is useful for screening agonists and
CC antagonists of HRIP polypeptide. HRIP and its agonist or antagonist
CC are useful for treating a disease or condition associated with
CC decreased or increased expression of functional HRIP. Diseases treated
CC or diagnosed include neurological disorders such as stroke, Parkinson's
CC disease, demyelinating diseases, bacterial and viral meningitis and
CC other developmental disorders of the central nervous system,
CC neuromuscular disorders, myasthenia gravis, cell proliferative disorders
CC such as actinic keratosis, arteriosclerosis, atherosclerosis and cancer
CC including leukemia, melanoma, myeloma and cancer of the adrenal gland,
CC bladder, bone, bone marrow, liver, lung, muscle, ovary, autoimmune/
CC inflammatory disorder such as Addison's disease, acquired
CC immunodeficiency diseases, allergies, bronchitis, diabetes mellitus,
CC rheumatoid arthritis, microbial infection and trauma.
XX
SQ Sequence 485 AA:

Query Match 89.0%; Score 2470; DB 21; Length 485;
Best Local Similarity 99.6%; Pred. No. 1,46-184;
Matches 462; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Oy 55 KAISREYAAASLDNFEVLTLEGEVYKVMDDPKPALVTKFMKNGSISGLDSQCFRP 114
Db 22 kaisreykamasldnfevltlegevykvmddpkpalvtkfmngsisglisqcfprp 81
Oy 115 PLICRLAKFVYLKGFYIHONPVYLHROLKPSNVLPBELVYKADRGSLTFGGSGOSGT 174
Db 82 plicrlakfvyllkgnpvyllhrodkpsnvlldpelnvkladrgslctfgsgsgsgt 141

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OY 175 GSGEPGIGLGYLAPELFVNVRKASTASDVSSGILMNAVLAGREVLPTEPSLYEAVC 234
DB 142 GSEPPGTLGYLAPELFVNVRKASTASDVSSGILMNAVLAGREVLPTEPSLYEAVC 201
OY 235 NQNRSLAELEQAGREPPGLEGLEKLNQLMSESPDRSPFQCLPRTDEVQVQENNM 294
DB 202 NQNRSLAELEQAGREPPGLEGLEKLNQLMSESPDRSPFQCLPRTDEVQVQENNM 261
OY 295 NNAVSVKRFSLQSLSSNRFSIPESGCGTENDGFRRTIENGRNDVNSFNKLNL 354
DB 262 NNAVSVKRFSLQSLSSNRFSIPESGCGTENDGFRRTIENGRNDVNSFNKLNL 321
OY 355 EEPSSVPRKCPSTLRKSHAOEYVQAMTAGSSDSMAQPPQTPETSTFRNQMPSTST 414
DB 322 EEPSSVPRKCPSTLRKSHAOEYVQAMTAGSSDSMAQPPQTPETSTFRNQMPSTST 381
OY 415 GPPSPRQNGABERQNMNSCRTEPPRYTGRPLVNIYNSGVQVGDNNYLTMOQTAL 474
DB 382 GPPSPRQNGABERQNMNSCRTEPPRYTGRPLVNIYNSGVQVGDNNYLTMOQTAL 441
OY 475 PRMGLAPSGKGLQHPPRYVGSQEGPRKPMASRPCKMYNRSGK 518
DB 442 PRMGLAPSGKGLQHPPRYVGSQEGPRKPMASRPCKMYNRSGK 485

RESULT 13
AAV45047
ID AAV45047 standard; Protein: 437 AA.
AC AAV45047;
XX 31-MAY-2000 (first entry)
DE Human Apop3 (82-518) truncation mutant.
XX
KW Apop3 truncation mutant; Apop3 protein; apoptotic protein; cytostatic;
KW immunotherapy; RIP3; receptor-interacting protein; apoptosis modulation;
KW apoptosis-mediated disorder; TNFalpha-induced caspase activation;
KW cancer; autoimmune disorder; cytostatic; degenerative disorder;
KW viral infection; cell loss; inhibitor of apoptosis protein; IAP;
KW TNFalpha signalling complex; tumour necrosis factor.
XX
OS Homo sapiens.
XX
PN WO200007545-A2.
XX
PD 17-FEB-2000.
XX
PE 06-AUG-1999; 99WO-US17776.
XX
PR 06-AUG-1998; 98US-0095587.
PR 06-AUG-1998; 98US-0095590.
PR 08-SEP-1998; 98US-0099486.
XX
PA (RIGI-) RIGEL PHARM INC.
XX
PI Luo Y, Huang BCB, Shen M, Yu PW;
XX
DR WPI: 2000-205547/18.
XX
PT Novel apoptotic proteins Apop1, Apop2 and Apop3 and recombinant nucleic
PT acids encoding them for use in screening modulators which is useful for
PT diagnosis and treatment of diseases
XX
PS Example 2: Page: 64pp; English.
XX
CC The patent discloses the use of novel apoptotic proteins and related
CC molecules involved in apoptosis modulation. Expression vectors
CC comprising the Apop DNA can be used to transform host cells. Apop DNA
CC can be administered as DNA vaccines. Apop proteins are used to make
CC polyclonal and monoclonal antibodies for use in immunotherapy. The
CC proteins are useful in treating apoptosis-mediated disorders including

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CC cancer, autoimmune disorders, sustained viral infection, inappropriate
CC cell loss and degenerative disorders. Drug candidates that affect Apop
CC bioactivity are identified by screening. The present sequence is a
CC truncation mutant of Apop3 (82-518) protein, also known as RIP3
CC (receptor-interacting protein). This was used in experiments to
CC demonstrate activation of cellular caspases and NF kappaB (nuclear
CC factor kappaB). This N-terminal deletion mutant was able to activate
CC caspase activity and induced higher luciferase activity than full length
CC Apop3. The results indicated that Apop3's kinase activity is not
CC required for caspase activation. NF kappa B activation and cell death.
CC Note: The present sequence is not given in the specification but is
CC derived from Apop3 protein (AAV45042).
XX
SQ Sequence 437 AA;
Query Match 85.0%; Score 2357; DB 21; Length 437;
Best Local Similarity 100.0%; Pred. No. 8,4e-176;
Matches 437; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 82 VNMOPDRPALYTRFENSGISGLQSCPRPWLICRLKEVYLGMYLHONPVLLHR 141
DB 1 VNMOPDRPALYTRFENSGISGLQSCPRPWLICRLKEVYLGMYLHONPVLLHR 60
OY 142 DLKPSNVLPPDELVRKLAIDFGLSFGSGSGSGSGEGCTLCYLAPELFVNVRKASTA 201
DB 61 dlkpennlpdpelhvkladfglsfgsgsgsgsgsgsgsgsgsgsgsgsgsgsgsg 120
OY 202 SDVYSGILMNAVLAGREVLPTEPSLYEAVCNORNPRLAELPQAGETPGLEKLEL 261
DB 121 sdvysfgilnmavlagrevlptepsllyeavcnrnprrlaelpagsetpgleglkel 180
OY 262 MQLCMSSEPPKDRSPFQCLPRTDEVQVQENNMNAVSTKDFSLQSSNRFSIPESG 321
DB 181 mqlcmsseppkdrspfqclpkrdevfqvnenmaavstkdflsqssnrrtssipsag 240
OY 322 QGCTENDGFRRTIENGRNDVNSFNKLNLSEPPSVPRKCPSTLRKSHAOEYVQ 381
DB 241 qgctemdgfrtlenghsrndvnsfnklnleppsvprkcpstlkrshageevpq 300
OY 382 AWTAGTSSDSMAQPPQTPETSTFRNQMPSTSTGTPSPGRQNGABERQNMNSCRTEP 441
DB 301 awtagtssdsmaqppqpetslfrnqmpststgtpspgrngabergnmwscrtpep 360
OY 442 NPVTGRPLVNIYNSGVQVGDNNYLTMOQTALPTWGLAPSGKGLQHPPRYVGSQEG 501
DB 361 npvtgrplvniynsgvqvdnnyltmqqtalptwglapsgkglqhpprvsgsgpx 420
OY 502 DPEASRPCKMYNRSGK 518
DB 421 dpeasrpckmynrsgk 437

RESULT 14
AAV45043
ID AAV45043 standard; Protein: 436 AA.
XX
AC AAV45043;
XX
XX 31-MAY-2000 (first entry)
XX
DE Human Apop3 (1-436) C-terminal truncation mutant.
XX
KW Apop3 truncation mutant; Apop3 protein; apoptotic protein; cytostatic;
KW immunotherapy; RIP3; receptor-interacting protein; apoptosis modulation;
KW apoptosis-mediated disorder; TNFalpha-induced caspase activation;
KW cancer; autoimmune disorder; cytostatic; degenerative disorder;
KW viral infection; cell loss; inhibitor of apoptosis protein; IAP;
KW TNFalpha signalling complex; tumour necrosis factor.
XX
OS Homo sapiens.
XX
PI Key Location/Qualifiers
XX
FH

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OM protein - protein search, using sw model

Run on: August 13, 2002, 21:16:13 : Search time 42.77 Seconds

(Without alignment)
1166.013 Million cell updates/sec

Title: US-09-762-491-6

Perfect score: 2774
Sequence: 1 MSCVKLMPSGAPALVISE.....PKDEANSRPGQWTHSGK 519Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

Database : PIR_71:*

1: PIR1:*\n2: PIR2:*\n3: PIR3:*\n4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	445.5	16.1	656	2 I49299	receptor interact
2	433	15.2	671	2 T09479	serine/threonine p
3	321.5	11.6	667	2 T47482	receptor-like prot
4	321	11.6	567	2 JCS957	transforming growt
5	320.5	11.6	606	2 JCS956	transforming growt
6	318.5	11.5	579	2 JCS955	transforming growt
7	314.5	11.3	847	1 A53800	receptor like prot
8	307	11.1	685	2 T48177	mixed-lineage prot
9	307	11.1	1029	2 H86179	receptor like prot
10	303	10.9	954	1 S68178	hypothetical prote
11	302	10.9	821	2 T48400	mixed-lineage prot
12	299	10.8	829	2 T07406	serine/threonine-p
13	299	10.8	848	2 H87950	probable protein k
14	299	10.8	855	2 T20082	protein f332.2 [1
15	298	10.7	613	2 T77483	hypothetical prote
16	298	10.7	900	2 T04839	receptor like prot
17	295.5	10.7	512	2 S21171	protein kinase hom
18	294.5	10.6	736	2 T05157	activin receptor s
19	294.5	10.5	963	2 T09911	protein kinase hom
20	290.5	10.5	513	1 JQ1486	activin receptor t
21	290.5	10.5	513	2 A39896	activin receptor t
22	290.5	10.5	513	2 I45850	activin receptor t
23	290	10.5	655	2 H96692	probable receptor
24	290	10.5	1171	2 T12956	hypothetical prote
25	289.5	10.4	513	2 A49193	type II activin re
26	289.5	10.4	513	2 S27258	activin receptor t
27	289.5	10.4	516	2 D84525	probable protein k
28	289.5	10.4	516	2 D84525	probable protein k
29	289.5	10.4	656	2 B86289	probable serine/th

30	289	10.4	627	1 JCS534	protein kinase 1 (
31	288	10.4	396	2 H86301	hypothetical prote
32	287.5	10.4	394	2 J00229	mixed-lineage prot
33	287.5	10.4	516	2 A48678	activin receptor t
34	287.5	10.4	682	2 T48175	receptor like prot
35	287	10.3	553	2 T04683	hypothetical prote
36	286.5	10.3	514	2 J01317	activin receptor p
37	286	10.3	1248	2 B96827	hypothetical prote
38	285.5	10.3	513	2 S23089	activin receptor t
39	285.5	10.3	669	2 T08960	serine/threonine-s
40	285.5	10.3	984	2 A39753	protein-tyrosine k
41	284.5	10.3	849	1 T09349	S-receptor kinase
42	284	10.2	567	2 H84770	probable receptor-
43	284	10.2	975	2 I48974	receptor-protein t
44	283.5	10.2	355	2 G96813	hypothetical prote
45	283.5	10.2	406	2 T52626	probable mitogen-a

ALIGNMENTS

RESULT 1
149299
receptor interacting protein R1P - mouse
C:Species: Mus musculus (house mouse)
C:Date: 09-Mar-1996 #sequence_revision 09-Mar-1996 #text_change 05-Nov-1999
C:Accession: I49299
R:Stanger, B.Z.; Leder, P.; Lee, T.H.; Kim, E.; Seed, B.
Cell 81, 513-523, 1995
A:Title: R1P: a novel protein containing a death domain that interacts with Fas/ADO-1.
A:Reference number: A56913, MID:95377838
A:Accession: I49299
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-656 <RSS>
A:Cross-references: EMBL:U25995; NID:g829618; PID:AB60487.1; PID:g829619
A:Genetics:
A:Gene: R1P
C:Superfamily: protein kinase homology
F:15-293/Domain: protein kinase homology <kin>

Query Match	16.1%	Score 445.5	DB 2	Length 656
Best Local Similarity	26.2%	Pred. No. 5.9e-14		
Matches 158	Conservative	89	Mismatches 205	Indels 151
Gaps				23
QY	15	LVYIEBLNDELIVGKDGPGVYRAOHRKRGVAVAKYIN-----SKATSRKYKAMASL 67		
DB	12	MASDLEKTDL-DSGGPKVSLCYHRSHGVILKVTGPNRAETVEVLEBGMKMRRL 70		
QY	68	DNEFVLRLDG-VIEKVMDDPPALVTKEMNGSLGGLASQCPRPWPLLCRLKREVL 126		
DB	71	RHSRYVLLDIIIEGNY-----SLVEYMEKMTLMVLTQIDVPLSLKGRHIVEALE 124		
QY	127	GMFLHDPNVPVLLHRLDKPSNVLPPELHVKLADRGSLTFQGGSG-----SGT 174		
DB	125	GMCLTHDKG-VIHKDLKENTILVDRPHIKADGVASFTHNKLKREKDNOKKVSST 182		
QY	175	GSGEPTGTLGLPELFAVNVNKRKASTASVYSFGILMAVLAGAEVETLPPEPLVTEAVG 234		
DB	183	TKRNGGTLLYMAPEHLINDIMAKPTEKSDVYSFGIVLWALPAKE---PRE-----NVIC 234		
QY	235	NRQ-----NRPDLAEIPQAGPETPGLEGKELMQLQNSSEKDRPSF---QECLEK 282		
DB	235	TEQFVICIKSGNPNVEIEILEYCPRE-----IISMERCHQAIREDRPFVGLIEBFRFP 289		
QY	283	TDEVF-QMVENNNMAAVSVYVKDFLSQKLSNNRPS-----IPES----- 320		
DB	290	YLSHFEEIVEDY---ASLAKETPQDSFYLDPMFSLOHDCVLPPLPSNSNEQGSLSHSSO 346		
QY	331	--GGGTENDGFFRTTENDSHRDVAVSEWLNK-----LNL 354		
DB	347	GLONGPVEESWFSSEYSPEDENDRSVQAKLQEEASYHATGIFAEKQTKRQPRONEAYNR 406		

QY 355 EEPSPSVPRKCKSLTKRSRAOEEOVPOAKTAG-----TSSDSMAQPPQTPETSTF-FRQ 407
DB 407 EERRRRKRSVSHDPFAOQRKA---ENKSKGANGSDPSTRTGAVDQLSHPTQTYWMNG 463
QY 408 MDSPTSTGTSPSPGPGNOCAGROGMNSCRTPEPN-----PYTGRPLVN-----IX 453
DB 464 LYNQMGFTGTGVMYPPMLSCMYSTYKTPYPTENIGSTPTMPYFSGPVADLLIKYTF 523
QY 454 NCSGVGVGNNTLTMOQTALPTWGLAPSCKGLQHPRPVGSOEGRPKDPEAMSRPGWY 513
DB 524 NSGCIQIGHNNTNDY-----GLNSQPRNTCK---EESTSRHQALF 561
QY 514 NNS 516
DB 562 DMT 564

RESULT 2
T09479
acoline/threonine protein kinase (EC 2.7.1.-) RIP - human
C:Species: Homo sapiens (man)
C>Date: 16-Jul-1998 #sequence_revision 16-Jul-1999 #text_change 17-Nov-2000
C:Accession: T09479; 138992
R:Huang, J.; Heu, H.; Balchwal, V. R.; Goeddel, D. V.
submitted to the EMBL Data Library, August 1998
A:Reference number: 216685
A:Accession: T09479
A:Status: preliminary; translated from GR/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-671 <HUN>
A:Cross-references: EMBL:U50062; NID:93426026; PID:93426027
R:Stanger, B. Z.; Leder, P.; Lee, T. H.; Kim, E.; Seed, B.
Cell 81, 513-523, 1995
A:Title: RIP: a novel protein containing a death domain that interacts with Fas/Apo-1
A:Reference number: A56913; MUID:95277838
A:Accession: 138992
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 300-513, 'S', 515-671 <RES>
A:Cross-references: EMBL:U25994; NID:9829616; PID:AA50137.1; PID:9829617
C:Genetics:
A:Gene: RIP
C:Keywords: ATP binding; phosphotransferase

Query Match 15.26; Score 423; DB 2; Length 671;
Best Local Similarity 25.36; Pred. No. 6.8e-13;
Matches 145; Conservative 95; Mismatches 186; Indels 146; Gaps 22;
QY 17 SIELENDLVKDGFGVFPRAQHRKMG-----YDVAVKIVNSKRAISREVKAMASLDN 69
DB 14 SDDPLESABL-DSGGFGKVSILCFHRTGOLIMIKTVYKGPACIHNELALEAKMNNRLRH 72
QY 70 EYVLRLEGVIEKVNMDOPKRALYTKPMENSGLSGLSCPPRWLLCLRLKLYVLCMF 129
DB 73 SKYVLLGVY-----IEGKYSLVMEIKENKMLNHYLKAENSTPLSKCRITLLEIBGC 127
QY 130 YLHDPNPVLLRDLKPSNVLPDELHYVLADFGISTGQSG-----SGTSG 177
DB 128 YLHGGC--VIRHDLKREHILVNDNFHKLADGLASFKMSKLNENHLEKREYGTAK- 184
QY 178 EPGGLGYLAPLELVNVRKASTADYVSGILMAVLAAGREVELPTESPVLYEAVCNRO 237
DB 185 KNGGTLTYMAPRLNDVNAKPTKSDYVSFAVYVMAIFAKE---PYE-----NAICGQ 236
QY 238 -----NRPSELAPQAGPRTGGLGKLEMLQCLMSSSPKRPSPQCLKRTDEVQ- 288
DB 237 LMKIKSKNRPVDDITETCPRE-----ITSLMKLCMEANPEKRPYF---PGIEKFRP 287
QY 289 -----VVENNMNAASVTRDFLSQKSSNRF-----SIPSS----- 320
DB 288 FYLSQLESVEEDVSLKREYSNEKAVYKRMOSIQIDLCVAVPSSRNSATEQPGSLHSQ 347

QY 321 --GCGTENDGFPRTIENQHSNDVMSSEH-----NKLNLKEPSPSVPRKC 365
DB 348 GLGKGPVSESMFAPSEHNPQEBNEPSLSKLDENANTHLGSKMDRQKOPKQVNAVNR 407
QY 366 PSLLTKRSRAOEEOVPA-----WTAGTSSDSMAQPP--POTPETSTFRN 406
DB 408 EE-ERRRRVSHDPFAOQRPEYENFONTEGKGTVSSAASMGNAVHPSPGLTSGQVLYQNN 466
QY 407 QMPS-----PSTGT-----PS-----PGRCNOGAGROGMNSCRTPEP 441
DB 467 GLYSNHFGRPLDPEGTAGPRVYRPIPSHNPISLHNIPYPERNYLGNTPTPPFSLEPTD 526
QY 442 NPVTGRPLVNYNCSGVGVGNNTLTMOQTAA 473
DB 527 ESKR-----YTIYNSTGIQIGAYNMEIGTSS 534

RESULT 3
T47482
receptor-like protein kinase - Arabidopsis thaliana
N:Alternate names: protein P18N11.180
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 02-Sep-2000
C:Accession: T47482
R:Jordan, N.; Bangert, S.; Wiedemann, R.; Voss, H.; Unseld, M.; Neues, H. W.; Lemcke, A.
submitted to the Protein Sequence Database, February 2000
A:Reference number: 224467
A:Accession: T47482
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-667 <JOR>
A:Cross-references: EMBL:AL132953
C:Genetics:
A:Experimental source: cultivar Columbia; BAC clone P18N11
A:Map position: 3
A:Note: P18N11.180
C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase hom

Query Match 11.6%; Score 321.5; DB 2; Length 667;
Best Local Similarity 32.5%; Pred. No. 3.6e-08;
Matches 103; Conservative 46; Mismatches 113; Indels 53; Gaps 14;
QY 26 LVYKDGFGVFPRAQHRKNGYDVAKIYV-----SKAISREVKAMASLDNEFLRLSGYI 79
DB 355 LVYKGGFGKVKYKGT-LPGSRHIAVRLSBDAGKQFYAEVYTMGNTOHRLVPLDGYC 413
QY 80 EKVWMDPPKRALYTKFMENSGLSG-LGQSCPRP-WPLLCRLLEVVYLGMYLHD-QNP 136
DB 414 RRRK-----ELLVSEYNSNGSLDOYLFYQNPSPGLQRIISLDIASALNYLHSGANP 468
QY 137 VLHRLDKPSNVLPDELHYVLADFGISTGQSG-----GSGSGSGGEGGTAGTAPLELVN 194
DB 469 AVLRHDKASNTWMLSDYKRGKRGDCAKAFQDPQGNLSNTAA---VGTIGMADEL---I 522
QY 195 NRRKASTADYVSGILMAVLAAGR---EVLPTESPVLYEAVCNQNRPSLAEL--PQAG 249
DB 523 RYTGSKRTDVALEFGLFLELYTCGRPEPELPQAKRYLVKVCCEMKKASLETLRDLKLG 582
QY 250 PE--TPGLELLEMLQCLMSSSEPRDPSFQCLPKTDEVGVYENNMNAASVTRDFLSQ 307
DB 583 REFLESEVEVYKLGILCTINDVPESRPD-----MGQVMTLSQ 620
QY 308 LKSSNRFSPESGCGC 324
DB 621 -KQLPDPSADSPGICG 636

RESULT 4
JC5397
transfoming growth factor-beta activated kinase (EC 2.7.-.-) 1c - human
C:Species: Homo sapiens (man)

C>Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 17-Mar-2000
 C/Accession: J05957
 R:Sakurai, H.; Shigemori, N.; Hasegawa, K.; Sugita, T.
 Biochem. Biophys. Res. Commun. 243, 545-549, 1998
 A:Title: TGF-beta-activated kinase 1 stimulates NF-kappaB activation by an NF-kappaB-Ind
 A:Reference number: J05955; MUID:9815801
 A:Accession: J05957
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-367 <SAK>
 A:Cross-References: DBJ:AB009358
 C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolo
 C:Keywords: phosphotransferase

Query Match 11.6% Score 321; DB 2; Length 567;
 Best Local Similarity 26.6% Pred. No. 3.2e-08;
 Matches 134; Conservative 77; Mismatches 182; Indels 110; Gaps 26;

OY 11 APAPLVSTIE-----ELENOELVKGDFGVFRADHRK--GYDAVATVNS-----KAISRE 60
 DB 21 APQVLFEEIDYKEIEVEEVGKAGFVCKA---KMRKDAVAIKQIESSEKRAFIYE 77
 OY 61 VKAMASIDNEFYLRLEGV-IEKVMNDODPKPALVTKEMENSLGSLQSCPR----- 113
 DB 78 LRQLSRVNHNPNVILKYLGAQLNPV-----CLVMEYAEGLSYNVLHGAEPPLPYTAH 129
 OY 114 ---WPLLCRLKLEEVYLGAFYLDONP-VLHRODKPSN-VLPPELVHVLADFG-----LS 164
 DB 130 AMSMCLQCS-----QGVATYLSMOPKALHRODKPNNLLVAGVTLKICDFGACDIO 183
 OY 165 TFOGSGSGTSGSEPGGTGLYAPLPELVNRRKASTADYVSGILMNAVLAGREV--EL 222
 DB 184 THMTNNK-----GSAMMAPEVFECSN--YSEKCDVFSMGIIMVEYTRRRPFDEI 232
 OY 223 PTEPSLVYEAVCNRRPSLAEI-POAGPETPGLGELKELQICMSSEPPDRSPDECT-- 280
 DB 233 GGPATFIMAVHNGTRPPLIKRLPR-----ISLMTKCMKSDPSQSPSMELIYKI 283
 OY 281 -----PKTDEVFQMV-----ENMNAVSTVKDFLSOLKSNRRFSIPESGGGTEH 327
 DB 284 MTHLMRYFPQADEPLQYPCQYSDGQSHAST--GSPNDIASTN-----TSNKSOTNM 335
 OY 328 DGFRRP-----IENQSHNDVMSSEMLKLEPPSSVPKRCP--SLTKRSRAQEOV 379
 DB 336 EQVPANNDITIKRLSKLKNQAKQOESGRSLGASGSSVESLPTPSCKRMSADNGBE 395
 OY 380 PQAWTAGTSSDSMAQPPQPTSTFRN--QMPSTSTGTSPSPRGNQGAERQGMNSCR 437
 DB 396 -EARIATTAISKPRKGR-KTASGNTLDVPELVISGNQPRRSIIDLTVTG----- 447
 OY 438 TPEPNEVTGR--PLVNIYNCSG 457
 DB 448 -TEPGVSSRSSSPSVRMITTS 469

RESULT 5

J05956
 transforming growth factor-beta activated kinase (EC 2.7.-.-) 1b - human
 C:Species: Homo sapiens (man)
 C>Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000
 C/Accession: J05956
 R:Sakurai, H.; Shigemori, N.; Hasegawa, K.; Sugita, T.
 Biochem. Biophys. Res. Commun. 243, 545-549, 1998
 A:Title: TGF-beta-activated kinase 1 stimulates NF-kappaB activation by an NF-kappaB-Ind
 A:Reference number: J05955; MUID:9815801
 A:Accession: J05956
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-606 <SAK>
 A:Cross-References: DBJ:AB009357; NID:92924625; PIDN:BA02026.1; PID:92924626
 C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolo
 C:Keywords: phosphotransferase

Query Match 11.6% Score 321; DB 2; Length 606;
 Best Local Similarity 26.6% Pred. No. 3.5e-08;
 Matches 134; Conservative 77; Mismatches 182; Indels 110; Gaps 26;

OY 11 APAPLVSTIE-----ELENOELVKGDFGVFRADHRK--GYDAVATVNS-----KAISRE 60
 DB 21 APQVLFEEIDYKEIEVEEVGKAGFVCKA---KMRKDAVAIKQIESSEKRAFIYE 77
 OY 61 VKAMASIDNEFYLRLEGV-IEKVMNDODPKPALVTKEMENSLGSLQSCPR----- 113
 DB 78 LRQLSRVNHNPNVILKYLGAQLNPV-----CLVMEYAEGLSYNVLHGAEPPLPYTAH 129
 OY 114 ---WPLLCRLKLEEVYLGAFYLDONP-VLHRODKPSN-VLPPELVHVLADFG-----LS 164
 DB 130 AMSMCLQCS-----QGVATYLSMOPKALHRODKPNNLLVAGVTLKICDFGACDIO 183
 OY 165 TFOGSGSGTSGSEPGGTGLYAPLPELVNRRKASTADYVSGILMNAVLAGREV--EL 222
 DB 184 THMTNNK-----GSAMMAPEVFECSN--YSEKCDVFSMGIIMVEYTRRRPFDEI 232
 OY 223 PTEPSLVYEAVCNRRPSLAEI-POAGPETPGLGELKELQICMSSEPPDRSPDECT-- 280
 DB 233 GGPATFIMAVHNGTRPPLIKRLPR-----ISLMTKCMKSDPSQSPSMELIYKI 283
 OY 281 -----PKTDEVFQMV-----ENMNAVSTVKDFLSOLKSNRRFSIPESGGGTEH 327
 DB 284 MTHLMRYFPQADEPLQYPCQYSDGQSHAST--GSPNDIASTN-----TSNKSOTNM 335
 OY 328 DGFRRP-----IENQSHNDVMSSEMLKLEPPSSVPKRCP--SLTKRSRAQEOV 379
 DB 336 EQVPANNDITIKRLSKLKNQAKQOESGRSLGASGSSVESLPTPSCKRMSADNGBE 395
 OY 380 PQAWTAGTSSDSMAQPPQPTSTFRN--QMPSTSTGTSPSPRGNQGAERQGMNSCR 437
 DB 396 -EARIATTAISKPRKGR-KTASGNTLDVPELVISGNQPRRSIIDLTVTG----- 447
 OY 438 TPEPNEVTGR--PLVNIYNCSG 457
 DB 448 -TEPGVSSRSSSPSVRMITTS 469

RESULT 6

T48176
 receptor like protein kinase - Arabidopsis thaliana
 N:Alternate names: protein F7A7.70
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C>Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 15-Sep-2000
 C/Accession: T48176
 R:Bevan, M.; Terry, N.; Ardiles, W.; Buysjaert, C.; Dasseville, R.; De Clerck, R.;
 ewes, H.W.; Rudd, S.; Lemcke, K.; Mayer, K.F.X.
 submitted to the Protein Sequence Database, March 2000
 A:Reference number: 224487
 A:Accession: T48176
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-688 <BEV>
 A:Cross-References: EMBL:AL161946
 A:Experimental source: cultivar Columbia; BAC clone F7A7
 A:Genetics:
 A:Map position: 5
 A:Note: F7A7.70
 C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase hom

Query Match 11.6% Score 320.5; DB 2; Length 688;

Best Local Similarity 31.4% Pred. No. 4.2e-08;
 Matches 101; Conservative 66; Mismatches 116; Indels 37; Gaps 15;

OY 22 ENOELVKGDFGVFRADHRKQVD-VAVKTVNSKAISREVKAMASIDNEFYLRLEGVIE 80
 DB 363 ENR-IVGTGFGVTFVGNLSSPSSDQIAVKKTPNSMGVREPIAEISIGRLRRKRLVN 421

OY 81 KVMN-DQPKPALVTKEMNGSLGLOSQCR-----PWLICRLKLEVLGMFLYLD 133
 DB 422 LOGCKCKMDLLIDYDIPKGLSLSLTSR-PROSGVVLNSMNRKFIAGISGLYLHE 480
 OY 134 Q-NPVLHRLDLPSPVLDLPELHKLADFGLS-TFQCSGSGTSGSEPGCTGLAPLE 191
 DB 481 EMEKVIYHRIIDIPSNVLIEDDMNPLGDFGLARLYERGOSQNT--TVVYCTIGYAPEL- 537
 OY 192 VVNNRASPASDYSFGILMNAVLAGREVELPEPSELVYA--VCNRNRPSEL--AELEQ 247
 DB 536 -ARNKSSASAPYFAFGVLLLEIYSGR---PTDSGTFILADVMELHARGLIAYDPR 593
 OY 248 APPEPGLGLEKELM--OLCWSSEKDRPSQECLE-----PRTDEVQWENKNNNA 296
 DB 594 LDFGIDGVEARLALVGLLCHORPTSPSKRLVRLYLNGLDDVDPEIDMWISDSSMSD 653
 OY 297 AVSTVKDLSQLKSSNRRFSIP 318
 DB 654 LGSNFGYVSDRASS---SVP 672

RESULT 7

Transferring growth factor-beta activated kinase (EC 2.7.-.-) 1a - human
 C:Species: Homo sapiens (man)
 C:Date: 16-Jul-1999 #sequence, revision 16-Jul-1999 #text_change 21-Jul-2000
 C:Accession: J05955
 R:Sakurai, H.; Shigemori, N.; Hasegawa, K.; Sugita, T.
 Biochem. Biophys. Res. Commun. 243, 545-549, 1998
 A>Title: TGF-beta-activated kinase 1 stimulates NF-kappaB activation by an NF-kappaB-ind
 A:Reference number: J05955; MUID:98153801
 A:Accession: J05955
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-379 <SAR>
 A:Cross-References: DDBJ:AB009356; NID:92924623; PIDN:BAA32023.1; PID:92924624
 C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolo
 C:Keywords: phosphotransferase

Query Match 11.58; Score 318.5; DB 2; Length 579;
 Best Local Similarity 25.78; Pred. No. 4.3e-08;
 Matches 129; Conservative 74; Mismatches 165; Indels 133; Gaps 25;
 OY 11 AAPLVSTF-----ELENOELVKGDCGTVPRAOHRK--GYDAVATVNS---KAISRE 60
 DB 21 APSQVLTNEEIDYKEIEVEVVGAGFVCKA---KRAKDAIAIKQISESEKRAFTVE 77
 OY 61 VKAMASLDNEFLVRLGV-IEKVNMDOPRALVTKFMENGSLGLOSQCRP----- 113
 DB 78 LKRLSRVNHPIVTKLYGACLNPV-----CLVMEYASGGSILYVILHGAEPPLPYTAH 129
 OY 114 ---WPLICRLKLEVLGMFLYLDQNP--VLHRLDLPSPN--VLDPDELHVLADFG---LS 164
 DB 130 AASWGLQS-----QGVAYLHSMQKALHRLDLPNLLVAGGVLYLIDCFGRACDIO 183
 OY 165 TFQCSGSGTSGSEPGCTGLAPLELVNNAKSTASDYSFGILMNAVLAGREV--EL 222
 DB 184 THTNTNKK-----GSAAMAAPEVFGSV--YSEKCDVFSIGIILMTYIRRRPFDEI 232
 OY 223 PREPSELVAVCNRRNPSLAELPOAGPETPGLGLEKLELMQWSEPPDRPSQECLE-- 280
 DB 233 GGPARRIMAVHNGTRPPLINKLP-----IESLMTKMSNDPQORSMEIYKI 283
 OY 281 -----PKTDEVQWY-----ENMNAAVSTVKDLSQLKSSNRRFSIPESGGGTEM 327
 DB 284 MTHLMRTFFGADPELQYCOYSDGOSNSATST-----GSFIM 320
 OY 328 DGFRTIENQSRNDVNASEMLNKLNEEPPSS--VPKCPSLTKRSRAQEQVQAWTA 385
 DB 321 D-----IASTNTSNK-----SOTNMEQVPAITNDITKRLSESLKLNQAKQSGSGLSL 368

OY 386 GTSSDSMAOP-POTPETSTFRNOMPS-----PTSTGPPSPGPGNGCAEROGNNWSCRTP 439
 DB 369 GASRGSSVESLEPTSGKAMSDSEIARIAATNGPRRRSIDULTVYG-----T 421
 OY 440 EPNPVTGR---PLVNITYNCSG 457
 DB 422 EPGVSSRSRSPSVRMITTSQ 442

RESULT 8

A3800
 mixed-lineage protein kinase (EC 2.7.1.-) 3 - human
 N:Alternate names: protein kinase PTK1; protein kinase SPRK
 C:Species: Homo sapiens (man)
 C:Date: 10-Sep-1999 #sequence, revision 10-Sep-1999 #text_change 10-Sep-1999
 C:Accession: A53800; 158395
 R:Gallo, K.A.; Mark, M.R.; Scadden, D.T.; Wang, Z.; Gu, Q.; Godowski, P.J.
 J. Biol. Chem. 269, 15092-15100, 1994
 A>Title: Identification and characterization of SPRK, a novel src-homology 3 domain-c
 A:Reference number: A53800; MUID:94253068
 A:Accession: A53800
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-847 <GAT>
 A:Cross-References: GB:U07747; NID:9464027; PIDN:AA19647.1; PID:9464028
 R:Yang, Y.L.; Leung, I.W.; Heng, H.H.; Tsui, L.C.; Lassar, N.D.
 Oncogene 9, 1745-1750, 1994
 A>Title: MUK-3: Identification of a widely-expressed protein kinase bearing an SH3 do
 A:Reference number: 158395; MUID:94239754
 A:Accession: 158395
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-847 <NES>
 A:Cross-References: GB:L32976; NID:9488295; PIDN:AAA59859.1; PID:9488296
 C:Genetics:
 A:Gene: GDB:MUK3; PTK1; SPRK
 A:Cross-References: GDB:14755; OMIM:600050
 A:Map position: 11q13.1-11q13.3
 C:Superfamily: mixed-lineage protein kinase 3; protein kinase homology; SH3 homology
 C:Keywords: ATP; leucine zipper; phosphotransferase; serine/threonine-specific protei
 F:48-100/Domain: SH3 homology <SH3>
 F:115-383/Domain: protein kinase homology <RTK>
 F:123-131/Region: protein kinase ATP-binding motif
 F:403-434/Region: leucine zipper motif
 F:438-459/Region: leucine zipper motif
 F:468-482/Region: basic

Query Match 11.38; Score 314.5; DB 1; Length 847;
 Best Local Similarity 21.58; Pred. No. 1e-07;
 Matches 157; Conservative 90; Mismatches 221; Indels 261; Gaps 29;
 OY 4 VKLWPS-----GAPAP--LVSIELENOELVKGDCGTVPRAOHRKNGDYAVAI----- 51
 DB 92 VGIRPSNYVRGGPPRCPEVASFOELRLAEVYIGCGFAYGSGNR--GELVAYAKAROD 149
 OY 52 -----VNSAISREYKAMASLDNEFLVRLGVIEKVNMDOPKRALVTKFMENGSLG 105
 DB 150 PDEDISTASVYNOEARLFAMLAHPNIIALKAVCL-----EENLCLVMEYASGGSILSA 204
 OY 106 LOSQCPPEPPLICRLKLEVLGMFLYLDQNPV--LHRLDLPSPNVL-----PDELH--V 156
 DB 205 LAGRRVPP--HVLVNNAVQIARGMHYLCHEALVPIHRLDKSNHILLQPISSDDMBKTL 263
 OY 157 KLADFGLSTFGSGSOSGSGSEPGCTGLAPLELVNNAKST--ASDYSFGILMNA 213
 DB 264 KITDFGLAR-----EMHKTQMSAAGTYAMNAPEVI-----KASTSKSDVMSFGVILME 314
 OY 214 VLAGREVELPTEP---SLVLEAVCNRRNPSLAELPOAGPETPGLGLEKLELMQWSE 269
 DB 315 LILG---EYVYRICDLAVAVGAVVNTLTP---IPSCPPP-----PAQIMADCAQD 362
 OY 270 PKDRPSP-----GQCLPKTD 284

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DB 363 PRRPFPASILQOLEALNAOVLEKMPRDSFHSMOEGMKREIOGLFDELAKEREKILLSRE 422
QY 285 EFGQWENNNMNA----- 297
DB 423 ELFRARBEQSQAEOLRRREHLNQMELVEPERELTLLOQVDRERPHYRRRGTFKRSK 482
QY 298 -----VSTVKDFLSGL-----KSNRFFSTPESGCGT----- 325
DB 483 LRAADGERISMEDPKRITVQASPGDLRRRRNVEFGPDSPFPFRALQLEPAERQ 542
QY 326 -----EMDGFRT-----IENQSHNDVASEM----- 348
DB 543 AMGRSPRLLEDSONGERACVAMGSPFKPGEAQNRRRSRDDEATVTLDSDDSPG 602
QY 349 -----LN-----KUNLEEPSSTPKR-----CPSTLRSAQEDQVPAWTKGTS 390
DB 603 PSTPPALNGNPPRPSLEPERKRPVPAKSSGSGTFLIGRALLR-----GTALLSLG 658
QY 391 SMAQPPQTESTFRNQMSPTSTGTPRPGNCGAERQGMMSCTPEPMPVTGRPLV 450
DB 659 RDQPPGCGP-----RERGSPPTPTPTPAPCPTEPPSPPLICFSIKTDSPTAPALL 714
QY 451 NINCSGVQVGNVLTLMQOT-----TALPTMGILAPSGKR-GIQHPPPVSGSGPRDP 503
DB 715 DL-----GIVGQSAKSPRREREPRGCVSPPTGSAATCTGTPTSPPLILSRP 770
QY 504 EAMSPQGW 512
DB 771 PLRSRIDPW 779

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RESULT 9
T48177
receptor like protein kinase - Arabidopsis thaliana

N:Alternate names: protein F7A7 80
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 15-Sep-2000
R:Accession: T48177
R:By: Van, M.; Terry, N.; Ardiles, W.; Buysaert, C.; Dasseville, R.; De Clerck, R.; De
Smet, H.W.; Rudo, S.; Lemcke, K.; Meyer, K.F.X.
Submitted to the protein sequence database, March 2000
A:Reference number: 224487
A:Accession: T48177
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-685 <BEV>
A:Cross-references: EMBL:AL161946
A:Experimental source: cultivar Columbia; BAC clone F7A7
A:Genetics:
A:Map position: 5
A:Note: F7A7 80
C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolog

Query Match 11.1%, Score 307, DB 2, Length 685;
Best Local Similarity 30.0%, Pred. No. 1, 8e-07;
Matches 99: Conservative 64: Mismatches 115: Indels 52: Gaps 14:

```

DB 19 ELENDELVKXGPGFVPAQHRKMGIVANKYNSKAI-----REYKMAASLDNERV 72
QY 355 EGKERNVVGTCGFCIVTGRIRSSDQIAVKITTPNSMGVREVAETESIGRLRHNL 414
DB 73 LRLEGVIEKVNMDQPKPALVTKFEMNGSLGLOSQCP-----PAPLRLRLKEVYL 126
QY 415 VNIQGCGRHN-----DLLLITDYIPNGSLDLSLXK-PRRSGAVLSMNAFOIAKGIAS 468
DB 127 GMYFLIDQ-NPVLRLKRLKPSNVLPDPDLHYKLADFLS-TFGGSGSGSGGEGCGTIG 184
QY 469 GLYLHEBQIVYHRDVPNSVNLDSQNRDLDFLALYKSGSGCT--TVYVGTIG 526
DB 185 YLAPLFPVNNRKASVDSVSGTLMNAVLAGEVELTPELVELYEAQCNRRNPISAE 244
QY 185 YLAPLFPVNNRKASVDSVSGTLMNAVLAGEVELTPELVELYEAQCNRRNPISAE 244

```

```

DB 527 YMAELARNGN--SSASDVFAFGVLLLEIVSGRK---PTDSGTFIA-----DWNE 574
QY 245 LPQAPETPL-----EGLKELM-----QLCMSSSPKDRSPQECPLP--KTDEVDM 289
DB 575 LQASGELSLADRLGSGVDEGEARLALAVGLCOHMKPESRPLMYLVLYLRDEVDPE 634
QY 290 VENNMAAVSTVDFLSQK-----SSNRFS 316
DB 635 IHDNMGYSDDSKTDLSKLVGYISSDRASS 664

```

RESULT 10

H86179
hypothetical protein [imported] - Arabidopsis thaliana.

C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
R:Accession: H86179
R:By: Chou, J.; Ecker, J.R.; Palm, C.J.; Federapfel, N.A.; Kaul, S.; White, O.; Alon
Chen, C.W.; Hughes, B.; Huizer, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Rhykin, E.; Kim,
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Malt, R.; Morzila
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shlun, P.; Southwick, A.M.; Sun, H.; Tallon
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A>Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719
A:Accession: H86179
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1029 <STOD>
A:Cross-references: GB:AE005172; NID:G2494111; PIDN:AAB80620.1; GSPDB:GN00141
A:Genetics:
A:Map position: 1

Query Match 11.1%, Score 307, DB 2, Length 1029;

Best Local Similarity 32.1%, Pred. No. 2, 7e-07;
Matches 100: Conservative 49: Mismatches 103: Indels 60: Gaps 13:

```

DB 9 SGAPAPVLSIE-----ELENDELVKXGPGFVPAQHRKMGIVANKYNSK 55
QY 726 SFSEMAVREIAGITGIIKTKMDLHELGSFGFVY--YGNRGDVAIKRIRKS 782
DB 56 AIS-----REVMAASLDNERVLEGVTEKVNMDQPKPALVTKFEMNGS 101
DB 783 CFSGGSSEQARQKTKDWRKARILANLHNRVNAVTFVPPD---GPGTMAVTEIVYNS 839
QY 102 LSGILSQCPRPPLLCRLKLEVLGMFTLHDQNPVLLRLKPSNV--LPDPDLHY-K 157
DB 840 LRHQLQK-DRRRKIMITY--DSARGMEYLRHKN--IVHFDLKCNDLVNLRDPPRICK 894
QY 158 LADGLSTFGGSGSGSGSGSGSGTGLYLAPELVNVRKASVDSVSGTLMNAVL 217
DB 895 VGDGSLRIR--RNLTVSGVGTGLPMAPLGLNGSSNRVSEKVDVSGIYMEILLG 951
QY 218 RE-----VELTRESLYLVAVCNQRNPISAELEPQAGETGJLSKIMDLQCSSSP 270
DB 952 EEPYANLHCVFEDDELGSFGGIVNNLTLPVPERCA-----EMKRLDQCSFDP 1003
QY 271 KDRSPQECPLP 282
DB 1004 GVRPSFEIYER 1015

```

RESULT 11

S68178
mixed-lineage protein kinase 2 (EC 2.7.1.-) - human

C:Species: Homo sapiens (man)
C>Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 11-Jun-1999
R:Accession: S68178; I38044; S32468
R:Dorov, D.S.; Devereux, L.; Tu, G.F.; Price, G.; Nicholl, J.R.; Sutherland, G.R.; Si

Bur. J. Biochem. 234, 492-500, 1995
 A>Title: Complete nucleotide sequence, expression, and chromosomal localization of human
 A:Reference number: 568178; MUID:96128179
 A:Accession: 568178
 A:Molecule type: mRNA
 A:Residues: 1-954 <DOR>
 A:Cross-references: EMBL:X90846; NID:9971419; PIDN:CAA6351.1; PID:9971420
 R:Kato, M.; Hirai, M.; Sugimura, T.; Terada, M.
 Oncogene 10, 1447-1451, 1995
 A>Title: Cloning and characterization of MST, a novel (putative) serine/threonine kinase
 A:Reference number: 138044; MUID:9524256
 A:Accession: 138044
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-461, 'A', 'V', '465-470', 'S', '472-806', 'R', '808-817', 'A', '819-954 <RES>
 A:Cross-references: EMBL:Z48615; NID:9758592; PIDN:CAA8531.1; PID:9758593
 R:Drory, D.S.; Devereux, L.; Dietzsch, E.; de Kretser, T.
 Eur. J. Biochem. 213, 701-710, 1993
 A>Title: Identification of a new family of human epithelial protein kinases containing
 A:Reference number: S32467; MUID:93238756
 A:Accession: S32468
 A:Molecule type: mRNA
 A:Residues: 244-464, 'AQAAGKRPQHPALML' <DOR>
 C:Genetics: GDB:MLK2; GDB:MST
 A:Gene: GDB:MLK2; GDB:MST
 A:Cross-references: GDB:362654; GDB:624810; OMIM:600317
 A:Map position: 19q13.1-19q13.2
 C:Superfamily: mixed-kinase protein kinase 2; protein kinase homology; SH3 homology
 C:Keywords: ATP; leucine zipper; phosphotransferase; serine/threonine-specific protein
 F:23-76/Domain: SH3 homology <SH3>
 F:104-112/Region: protein kinase homology <KIN>
 F:104-112/Region: protein kinase ATP-binding motif
 F:384-405/Region: leucine zipper motif
 F:419-440/Region: leucine zipper motif
 F:449-463/Region: basic
 F:125,145,222,224/Active site: Lys, Glu, Asp, Lys status predicted

Query Match 10.9%; Score 303; DB 1; Length 954;
 Best local similarity 22.8%; Pred. No. 3.9e-07;
 Matches 150; Conservative 85; Mismatches 223; Indels 200; Gaps 32;

DB 4 VILMP-----GAPRLVSI-----ELENOELVGKGGCTVRAQHRKMGIDAVK 50
 DB 68 VQVPSNVYAPAPAPAGLDLQDEIRPEHQLDEIIGVGFGRVRLMR--GEVAVK 125
 DB 51 -----IYNSKAISREYKMAASLDNEFVRLGCVIKVMDDPKPALVTKFMENG 100
 DB 126 AARLDPEKDPATVAQVQEARLFGALQHPNIIALRGACL-----NPHLCVINEYARAG 180
 DB 101 SLSGLSQSCPRPMPILRLKLEVTYGMFYLDHNPV--LHRDLKPSN--VLPEELH-- 155
 DB 181 ALSRVLAGRRVP--HVLVNNVAVYARGMNYLNDAPPIIHRDLKSLNILLLEALENNRL 239
 DB 156 -----VRLDFGLSTFGQSGSGSGGCGTGLYLADE-----LFPVNRKASVSDVYS 206
 DB 240 ADTVLKLTFDEGLAR---EMHKTTRKMSAAGVYAMAEVRLSLF-----SKSDVMS 288
 DB 207 FGILMAVLAG----REVELPTEPSLYEAVCNRNRPRLAELPOAGPETPGLEGKELM 262
 DB 289 FGVLLMELLTGEVPREID---ALAVAYGVAMNKLTP---IPSCPRP-----FARLL 336
 DB 263 QLCNSSEPRKDRSPQECPLKTD-----EVQNYENMNAVSTVDEL-----S 306
 DB 337 EECMDPDRIGRDFGSLILKLEVTIDQSLFQMPLESHSHSLQEDMKLEIOMHMDLTKRK 396
 DB 307 QKSSNRPSIPESGQGTEDKGFRTIENSHNDVNSE---MINKLLEP----- 357
 DB 397 ELRSREELRLAAQGRQEQRLRRRDELAREMDIVRELLILMLCQSLQSKPRVRKK 456
 DB 358 -----PSSVPRK-----CPSLTKRSRAQEDVPAQNAAGSSSM 392
 DB 457 GMPKRSRLKLRLDGSNLSLPSGFEHKTLYQASFTLDKR-----GSDG- 500

DB 393 AQPEQRE-TSTRNQMSPSTGTSPSC-----PRGNO--GAERGNMWS 435
 DB 501 ASPSPSIIPRLAIRLTPVCCGSSSSSGSGTWSRGPPKKEELVGGKKGRATWG 560
 DB 436 -CRPEPNPVGARPLVNIYNGVQGNNTLTWQOTLALPTGLAP----- 481
 DB 561 PSLRLKERVGGSE-----RLKGLDEG-----SKWSSAPNIGKSPKRTPIAPQFASLN 610
 DB 482 -----SGKRGQLQHP-----PVSGDSGRPDPEAW-----SRPGGVNRSCK 518
 DB 611 EKESPAEDGGSSVPPSPYSTPSTLSVLPFAEPSGAPARAFNPPTSPAPRNHGARG 668

RESULT 12
 T84800
 serine/threonine-protein kinase ctrl - Arabidopsis thaliana
 N:Alternate names: protein F17C15.150
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 20-Apr-2000 #sequence--revision 20-Apr-2000 #text_change 17-Nov-2000
 C:Accession: T84800; A45178
 R:Bevan, M.; Pohl, T.; Weizenegger, T.; Bancroft, I.; Mewes, H.W.; Rudd, S.; Lemcke,
 submitted to the Protein Sequence Database, March 2000
 A:Reference number: 224492
 A:Accession: T84800
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-821 <BEV>
 A:Cross-references: EMBL:AL162506
 A:Experimental source: cultured Columbia; BAC clone F17C15
 R:Kieber, J.J.; Rothenberg, M.; Roman, G.; Feldmann, K.A.; Ecker, J.R.
 Cell 72, 427-441, 1993
 A>Title: CTRL, a negative regulator of the ethylene response pathway in Arabidopsis,
 A:Reference number: A45178; MUID:93161417
 A:Contents: Columbia
 A:Accession: A45178
 A:Status: preliminary; not compared with conceptual translation
 A:Molecule type: DNA
 A:Residues: 1-468,470-821 <KIE>
 A:Note: sequence extracted from NCBI backbone (NCBI:124878)
 C:Genetics:
 A:Map position: 5
 A:Insertions: 216/31 317/2; 364/3; 399/2; 468/1; 560/1; 573/3; 596/3; 630/2; 658/3; 691/
 A:Note: F17C15.150
 C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase hom
 C:Keywords: ATP
 F:549-812/Domain: protein kinase homology <KIN>
 F:557-565/Region: protein kinase ATP-binding motif

Query Match 10.9%; Score 302; DB 2; Length 821;
 Best local similarity 33.6%; Pred. No. 3.7e-07;
 Matches 92; Conservative 44; Mismatches 96; Indels 42; Gaps 12;

DB 20 ELENOELVGKGGCTVRAQHRK--GIDVAVKYNK-----AISRYKMAASLDNE 70
 DB 550 DLNKEIGAGSGFYHRAE--NBSQVAKILMEQDPHAERWFEFLKVAIMRLNHP 606
 DB 71 FVRLGCVIKVMDDPKPALVTKFMENGSLGLOSQSCPRPMPILRLK--EYVLG 127
 DB 607 NIVLFMGAV----TPRPMLSTVEYLSRGSLYRLHKSGARQDLERRRLSMADVAKG 661
 DB 128 MFVLDHNPVTLRLDKPSNVLPEELHVKLADRGSLTSGGSGSGSGSGGCGTGLYLA 187
 DB 662 MNYLHNNRPVYHRDLKSPNLLVDKKTIVKVCDFGLSRLL--ASTFLSKSAAGPEKMA 719
 DB 188 PELFVNNRKAASVSDVYSFGILMAVLAGREVELPTEPSLYEAV--CNRNRPSLAE 244
 DB 720 PE--VLRDESNKSDVYSFGVILMELATLQDPFGNLPAAQVAVGVGCKR-----LE 771
 DB 245 LPO-AGPETPG--LEGKELMDLQNSSEPKDRPSF 276
 DB 772 IPRULAPQVAAITEG-----CYNTEPKRPSF 798

RESULT 13
 T07406
 C:Species: Lycopersicon esculentum (tomato)
 C:Date: 1-May-1999 #sequence_revision 14-May-1999 #text_change 08-Oct-1999
 C/Accession: T07406
 R:Wang, Y.
 submitted to the EMBL Data Library, May 1997
 A:Reference number: 216016
 A:Accession: T07406
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-829 <MAN>
 A:Cross-references: EMBL:Y1373; NID:01050452; PIDN:CA137322.1; PID:0334294
 A:Experimental source: strain UC828; sub.species Mill
 C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolo

Query Match 10.9%; Score 302; DB 2; Length 829;
 Best Local Similarity 31.8%; Pred. No. 3.7e-07;
 Matches 102; Conservative 44; Mismatches 103; Indels 72; Gaps 15;

25 ELYGKGGFETVRADHRRK-GDVAVKTV-----NSRAISREVKAMASDNEFVRL 75
 DB 559 EKIGAGSFGTVHRGD---WHSQVAVKILMKQDFHAEKLEFLEVALIKRLHPRIYLF 615
 OY 76 EGVIERVNDQDQKPAVTKFENSGSLGLOSQCP---PWPILCRLLKEVILGMYL 131
 DB 616 MCAV-----IOPNLSIVTEYLSRGLRILMKGAREVLDERRLC-NAVAVANGMYL 669
 OY 132 HDQNPVLRDLKPSNVLPDELAHYKLADFGISTFGGGS--QSGTSGGPGGTGLAYLE 189
 DB 670 HKNRPPIVARDLKSPLYLDKRYTKICDFLSRFKANTLSKTAAGTP---EMWAP 725
 OY 190 LFTVNRKASTASDVYSGIILMAVLAGREVELFTEPSIYEVY-CNQRNRSIAEL-PQ 247
 DB 726 --VIRQPSKESDVYSFVILMELATLQDQPMKMLNPQVIAVGRKRLDIPSLNPQ 783
 OY 248 AGPEVGLGLKELMQLCWSSEPKDRPSFQDCLPKTDEQVENNMMAVSTVDFL-S 306
 DB 784 -----VAIIIEACWANEPMKRPSE-----STINDMLRP 811
 OY 307 QLKSNRRFSIPESGGCGTEM 327
 DB 812 HLKS-----PLPPGHDM 825

RESULT 14
 B87930
 C:Species: Caenorhabditis elegans
 C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 10-May-2001
 C/Accession: B87930
 R:anonymous, The C. elegans Sequencing Consortium.
 Science 282, 2012-2016, 1998
 A:Title: Genome sequence of the nematode C. elegans: a platform for investigating biolog
 A:Reference number: N75000; MIM:99065613; PMID:9851916
 A:Note: See web site genome.wustl.edu/gsc/C.elegans/ and www.ganger.ac.uk/projects/C_ele
 A:Note: Published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and
 A:Accession: B87930
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-848 <STO>
 A:Cross-references: GB:chr_I; PIDN:CA06544.1; PID:g3876653; GSPDB:GN00019; CESP:F33E2.2
 C:Genetics:
 A:Gene: F33E2.2
 A:Map position: 1

Query Match 10.8%; Score 299; DB 2; Length 848;
 Best Local Similarity 27.0%; Pred. No. 5.3e-07;

Matches 128; Conservative 66; Mismatches 200; Indels 80; Gaps 21;

5 KLWPSGAPPLVSTIELENOELCVGKGGFETVRADHRRKGGDVAVKTVNSKAISREVKAM 64
 DB 53 ELW-----EIPDAISEL-----EWLGSSGCAVPRGLE--NRTVAVKVN-QLAETETIKHL 102
 OY 65 ASLDNEVRLAEVIERVNDQDQKPAVTKFENSGSLGLOSQCPWPVILCRLLKEV 124
 DB 103 RHLRNONIIEFLGVCSR-----SPCYIMECSKRGQLCTVLSKRNITRELAQWVKEI 157
 OY 125 VLGFYVLDQNPVLRDLKPSNVLPDELAHYKLADFGISTFGGSGSGTSGEPGCTGL 184
 DB 158 ADGNHILH-QNWK-IHRDLKSPNIIASAEDSIKICDFGISHMKKMDSTWMSF--CGTWS 213
 OY 185 YLAPLELVN--VNRKASTASDVYSGIILMAVLAGREVEL--TEPSIYEVACNQNRP 240
 DB 214 WMAPDKIKQPCNEKY----DIVSFGVLMELT--REPIYANIMAAITIGVGTNLSLP 268
 OY 241 SLAELPQAGPETGLGLKELMQLCWSSEPKDRPSFQDCLPKTD---EYQVVENNMNA 296
 DB 269 -----MPEBAP-----KGLVLLIKOCISQKGRNRPFSIHRQWEIFRPELFEMTEEBMDL 319
 OY 297 AVSTYNDPLS--OLKSNRR-----FSIPESGGG-----TEMQGFRTYENQSHN 341
 DB 320 AMDSTRERACIOYPTVTRDNGRPSAFAMEEIQRRHOLHIIDIRNMEKILKRT 379
 OY 342 DVM-----VSEMLKNTLEEPSVVRKCPSLTKSRQAEQVPOART 384
 DB 380 NKMDKILQCGFTEIKELKESELAEM--ENDLTEREQWANHNSPKVAAPRQALQGYPRGY 437
 OY 385 AGTSSDSMAQ-----PQTPETSTFRNQPSTSTGTPSPGRNOCAGROCNH 433
 DB 438 DQMSDEQVQPCRGSPYRCAGNTSSSGVQSPFSRSSRSSAGQRRREBZAN 491

RESULT 15
 T20082
 C:Species: Caenorhabditis elegans
 C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 29-Oct-1999
 C/Accession: T20082; T21703
 R:Lennard, N.
 submitted to the EMBL Data Library, April 1998
 A:Reference number: 219221
 A:Accession: T20082
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-855 <NHL>
 A:Cross-references: EMBL:A1022593; PIDN:CA18635.2; GSPDB:GN00019; CESP:F33E2.2
 A:Experimental source: clone C49G9
 R:Lennard, N.
 submitted to the EMBL Data Library, January 1997
 A:Reference number: 219461
 A:Accession: T21703
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-855 <N12>
 A:Cross-references: EMBL:284574; PIDN:CA06544.2; GSPDB:GN00019; CESP:F33E2.2
 A:Experimental source: clone F33E2
 C:Genetics:
 A:Gene: CESP:F33E2.2
 A:Map position: 1
 A:Introns: 47/2; 213/2; 263/2; 366/3; 494/1; 547/3; 608/1; 826/3

Query Match 10.8%; Score 299; DB 2; Length 855;
 Best Local Similarity 27.0%; Pred. No. 5.3e-07;
 Matches 128; Conservative 66; Mismatches 200; Indels 80; Gaps 21;

5 KLWPSGAPPLVSTIELENOELCVGKGGFETVRADHRRKGGDVAVKTVNSKAISREVKAM 64
 DB 53 ELW-----EIPDAISEL-----EWLGSSGCAVPRGLE--NRTVAVKVN-QLAETETIKHL 102

```

0Y 65 ASDJNEVLTBEVIERKVMMDPPRALVYTFEMENGLSTLSLOSCPRMPLILRLKEV 124
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 103 RHLRKHUHLIEELGVCK-----SPECILYMEYCKGKGLCVYKSRNTIRLFPQMVKEI 157
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
0Y 125 VLGHFYTHDQNPVLLHRDKLPSPNVLPDELVAKLADGLSTFDGGSQSSTGSGEPGTLG 184
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 158 ADGNHLYLH-ONKV-IHRDLSKPNLITSAEDSIKICDFGTHMOKKNDSTYMSF--CSTVS 213
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
0Y 185 YLABELPVN--VVRKASTADVYSGEILMAVLAGREVELP--TEPSLYEAVYCNORNP 240
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 214 WMAEENKKNOPCKENY----DYVSGEYVLEMIL-RETPLYANIAQVATIEFGVNTILSP 268
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
0Y 241 SLALPQAGETRGSLGKELMOLQMSSEPPDRSPQELPKND----EYRONYENMNA 296
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 269 -----MPEAP-----KGLVLLIKLOLSQKGNRRSPSHIOMHEIKPELEFMEKEENOL 319
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
0Y 297 AVSTVAKDLS--OLKSSNR-----FSIPESGGQG-----TEMDGERRTIENQSRN 341
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 330 AMDSYREFAPACIOYPTSTVRDHCGRKSAFAAEEBETIQKRHEQDLNHIKDI RNMYEUKLRT 379
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
0Y 342 DVM-----VSEMLNKANLREPPSSVPRKCPSELTRFSRPADEQVPAWMT 384
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 380 NKHYDKLGCGFTELKKESELAEM--EKDILREBQHNQNSPAAVAAPQALRGPIBEGY 437
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
0Y 385 AGTSSDSMAQ-----PPQPELSTIRNMQSPPTSTGTSPSGPFGNCGAEROGNN 433
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 438 DDMSSDDVDQPCRGSPYRCNSMTSSSSGVQSSPFRSSSSSSAGQDTRRSECAN 491
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```

Search completed: August 13, 2002, 22:09:22
Job time: 3189 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compaq Inc.

OM protein - protein search, using sw model

Run on: August 13, 2002, 22:06:33 ; Search time 66.69 Seconds
(without alignments)
1346.294 Million cell updates/sec

Title: US-09-762-491-6
Perfect score: 2774
Sequence: 1 MSCVKLMPSCAPPLVSTIELENOELVGKIDFGTFVRAQRKRGYAVATVNSKALISKE 519
.....PKDEAWSRQPGWYHNSGKT 519

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: SP-archaea:*
2: SP-bacteria:*
3: SP-fungi:*
4: SP-human:*
5: SP-invertebrate:*
6: SP-mammal:*
7: SP-mhc:*
8: SP-organella:*
9: SP-phage:*
10: SP-plant:*
11: SP-rodent:*
12: SP-virus:*
13: SP-vertebrate:*
14: SP-unclassified:*
15: SP-virus:*
16: SP-bacteriophage:*
17: SP-archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2770	99.9	518	4 Q9Y572	Q9Y572 homo sapien
2	1389.5	50.1	486	1 Q9Q6L0	Q9Q6L0 mus musculu
3	1367	49.3	478	11 Q9Z2F5	Q9Z2F5 talus norv
4	404.5	14.6	784	4 Q96T11	Q96T11 homo sapien
5	401.5	14.5	784	4 Q9H4D1	Q9H4D1 homo sapien
6	401.5	14.5	784	4 Q96K80	Q96K80 homo sapien
7	399	14.4	786	11 Q9ERK0	Q9ERK0 mus musculu
8	379	13.7	540	4 Q43353	Q43353 homo sapien
9	340	12.3	527	5 Q9SR87	Q9SR87 dictyostell
10	333	12.0	593	10 Q9H177	Q9H177 homo sapien
11	324.5	11.7	564	4 Q9H177	Q9H177 homo sapien
12	320.5	11.6	667	10 Q9M020	Q9M020 arabidopsis
13	318.5	11.5	491	4 Q9KZ70	Q9KZ70 homo sapien
14	318.5	11.5	491	4 Q9KZ70	Q9KZ70 homo sapien
15	318.5	11.5	491	4 Q9KZ70	Q9KZ70 homo sapien
16	317.5	11.4	977	5 Q9VW24	Q9VW24 drosophila

17	317	11.4	606	11 Q923A8	Q923A8 mus musculu
18	314.5	11.3	847	4 Q16584	Q16584 homo sapien
19	313	11.3	1054	10 Q9FKL3	Q9FKL3 arabidopsis
20	312.5	11.3	616	13 Q73613	Q73613 xenopus lae
21	311	11.2	847	10 Q93XL9	Q93XL9 rosa hybrid
22	310	11.2	773	10 Q9C902	Q9C902 arabidopsis
23	310	11.2	850	11 Q93V15	Q93V15 mus musculu
24	308	11.1	1148	5 Q93V15	Q93V15 mus musculu
25	308	11.1	1161	5 Q950N8	Q950N8 drosophila
26	307	11.1	685	10 Q9M019	Q9M019 arabidopsis
27	307	11.1	1029	10 Q23015	Q23015 arabidopsis
28	306	11.0	718	10 Q9LSR8	Q9LSR8 homo sapien
29	305.5	11.0	1066	4 Q9H2N5	Q9H2N5 homo sapien
30	304	11.0	806	10 Q9ZSD8	Q9ZSD8 lycopersico
31	304	11.0	829	10 Q9ZSD9	Q9ZSD9 lycopersico
32	303.5	10.9	608	10 Q9FPD4	Q9FPD4 arabidopsis
33	302	10.9	718	10 Q93ZK5	Q93ZK5 arabidopsis
34	302	10.9	829	10 Q24027	Q24027 lycopersico
35	301.5	10.9	763	10 Q9C903	Q9C903 arabidopsis
36	301.5	10.9	777	10 Q9C833	Q9C833 arabidopsis
37	299.5	10.8	1141	10 Q9LHP4	Q9LHP4 arabidopsis
38	299	10.8	855	5 Q01700	Q01700 caenorhabdi
39	298.5	10.8	478	4 Q9NTR4	Q9NTR4 homo sapien
40	298.5	10.8	566	4 Q9NTR2	Q9NTR2 homo sapien
41	298	10.7	613	10 Q9M1G4	Q9M1G4 arabidopsis
42	298	10.7	900	10 Q65474	Q65474 arabidopsis
43	296	10.7	451	4 Q9NTR3	Q9NTR3 homo sapien
44	296	10.7	539	4 Q9NTR1	Q9NTR1 homo sapien
45	295.5	10.7	512	13 Q9PSM0	Q9PSM0 xenopus lae

ALIGNMENTS

RESULT 1
ID Q9Y572 PRELIMINARY: PRT: 518 AA.
AC Q9Y572; 01-NOV-1999 (TRENBLER, 12, Created)
DT 01-NOV-1999 (TRENBLER, 12, Last sequence update)
DT 01-DEC-2001 (TRENBLER, 19, Last annotation update)
DE RIP-LIKE KINASE.
GN RIP3.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID:9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-99272740; PubMed-10339433;
RA Yu P.W., Huang B.C., Shen M., Quest J., Chan E., Xu X., Nolan G.P.,
RA Payan D.G., Luo Y.,
RT "Identification of RIP3, a RIP-like kinase that activates apoptosis
RT and NF-kappaB".
RL Curr. Biol. 9:539-542(1999).
DR EMBL: AP156884; AAD39005.1;
DR InterPro: IPR001245; Tyr_kinase.
DR Pfam: PF00069; PKINASE.1.
DR PRINTS: PR00109; TYRKINASE.
KW ATP-binding; Kinase; Transferase; Tyrosine-protein kinase.
SQ SEQUENCE 518 AA: 56901 MW: 38433CFFEBBD4151 CRC64;
Query Match 99.9%; Score 2770; DB 4; Length 518;
Best Local Similarity 100.0%; Pred. No. 5; 3e-208;
Matches 518; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MSCVKLMPSCAPPLVSTIELENOELVGKIDFGTFVRAQRKRGYAVATVNSKALISKE 60
DB 1 MSCVKLMPSCAPPLVSTIELENOELVGKIDFGTFVRAQRKRGYAVATVNSKALISKE 60

Qy	61	VANA.SLDNEFYLRGVEYKXNMDOOKPALYTKFMENGSLGJLJOSCCRPMPPLCRL	120
Db	61	VKMAASLDNEFYLRGVEYKXNMDOOKPALYTKFMENGSLGJLJOSCCRPMPPLCRL	120
Qy	121	LKEVYLGMEFYLDHNDENVLLHRDLKPSNYLDPDELHYKLADFGJLSTFOGSSOGTSGCEPG	180
Db	121	LKEVYLGMEFYLDHNDENVLLHRDLKPSNYLDPDELHYKLADFGJLSTFOGSSOGTSGCEPG	180
Qy	181	GTLGTYLAPLPEFYVNNKKAATASDAYSSEGIILKNAVLAGREYELPTEPSLYEAYCNRBNRP	240
Db	181	GTLGTYLAPLPEFYVNNKKAATASDAYSSEGIILKNAVLAGREYELPTEPSLYEAYCNRBNRP	240
Qy	241	SLAELPQACPEPTGCLBSGLLELMQLKWSSEPKDRSPFOECLPKTDEVFQMVENNNNAAVST	300
Db	241	SLAELPQACPEPTGCLBSGLLELMQLKWSSEPKDRSPFOECLPKTDEVFQMVENNNNAAVST	300
Qy	301	VKPELSQLKSSNNRFEIPISSGGGGIENDGFRRTIENHSHNDVYNSSEMLKNTLNEEPPSS	360
Db	301	VKPELSQLKSSNNRFEIPISSGGGGIENDGFRRTIENHSHNDVYNSSEMLKNTLNEEPPSS	360
Qy	361	VPRKCPSLYTRSPAQEEVYPOAMTACGTSOSSMAOPOTPEPSTFRNOMPSPSTGTSPSG	420
Db	361	VPRKCPSLYTRSPAQEEVYPOAMTACGTSOSSMAOPOTPEPSTFRNOMPSPSTGTSPSG	420
Qy	421	PRGNQAGERGMNMSCRTEPNPYVGRELVNIYNCSSGVQGDNIYLTMOQTALPTGTLA	480
Db	421	PRGNQAGERGMNMSCRTEPNPYVGRELVNIYNCSSGVQGDNIYLTMOQTALPTGTLA	480
Qy	481	PSGKGRGLDHPRVGSOEPRKPRKPMWSPGQWYNNHSK	518
Db	481	PSGKGRGLDHPRVGSOEPRKPRKPMWSPGQWYNNHSK	518

Q99ZL0	2	PRELIMINARY:	PTF;	486 AA.
ID	Q99ZL0;			
DT	01-MAY-2000 (TrEMBLrel. 13)	Created		
DT	01-MAY-2000 (TrEMBLrel. 13)	Last sequence update		
DT	01-DEC-2001 (TrEMBLrel. 15)	Last annotation update		
DE	RECEPTOR INTERACTING PROTEIN 3.			
GN	RIP3.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.			
OX	NCBI_Taxid=10990;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	Pardentk N.J., Donner D.B., Goehl M.G., Harrington M.A.;			
RT	Mouse Interacting Protein 3 Does Not Contain a Caspase-Recruiting or			
RT	a Death Domain but Induces Apoptosis and Activates NF-kappaB."			
RL	Mol. Cell. Biol. 19:0-0(1999).			
CC	-1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.			
DR	EMBL: AF178953; AAF0133.1; "			
DR	Interpro: IPR000719; Euk_plkase.			
DR	Interpro: IPR002290; Ser_thr_kinase.			
DR	Interpro: IPR001245; Tyr_plkase.			
DR	Pfam: PF00069; plkinase; 1			
DR	Pfam: PF00109; tyrkase.			
DR	PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.			
DR	PROSITE: PS00011; PROTEIN_KINASE_DOM; 1.			
DR	PROSITE: PS00108; PROTEIN_KINASE_ST; 1.			
DR	ATP-binding: Serine/threonine-protein kinase; Transferase.			
SQ	SEQUENCE 486 AA: 53336 MW; DD264E69187D3436 CnC64;			
Query Match	50.1%;	Score 1388.5;	DB 11;	Length 486;
Best Local Similarity	59.1%;	Pred. No. 3,6e-100;		
Matches 299;	Conservative 49;	Mismatches 130;	Indels 23;	Gaps
07	1	MSCKLPSAPR-PLVSTELKNDLWKGKGVRRQHRKMGVDVAIVNSKAISR	59	
DB	1	MSCKLPSAPR-PLVSTELKNDLWKGKGVRRQHRKMGVDVAIVNSKAISR	60	

[illegible]

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RESULT      3
ID 0922P5      PRELIMINARY;      PRT: 478 AA.
AC 0922P5:
DT 01-MAY-1998 (TREMBLrel. 10, Created)
DT 01-OCT-2001 (TREMBLrel. 18, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE HOMOCYSTEINE RESPONDENT PROTEIN KCTP2.
OS Rattus norvegicus (Rat).
OC Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_Taxid=10116;
RN
RP
RC SEQUENCE FROM N.A.
RC STRAIN=RISTAR KYOTO.
RA Chen K.H., Tang J.;
RT "A homocysteine-respondent gene cloned from WKY USNCS by differential
RT display."
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
CC 1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL, AF036537; AAD02059.2; -.
DR InterPro: IPR000719; Euk_pkinase.
DR InterPro: IPR002290; Ser_thr_pkinase.
DR InterPro: IPR001245; Tyr_pkinase.
DR pfam: PF00069; pkinase; 1.
DR PRINTS; PR00109; TYRKINASE.
DR SMART; SM00220; S_TKc; 1.
DR SMART; SM00219; TYKc; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP_1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM_1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST_1.
KW ATP-binding; Serine/threonine-protein kinase; Transferrase.
SQ
SEQUENCE 478 AA; 52234 MW; EDC6C280C594E1977 CRC64;

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OY 1 MSCVKLMPGAPGAP-PLVSIIELENGELVKGDFGCTVRAQHRMGVDAVAKIVNSKAISR 59
DB 1 MSSVKMLKMGASSISLYSGSEEELENGEFVKGDFGAVARRHTAMNDVAVAKIVNSKISR 60
OY 60 EVKAMASLNEFVLRLEGVIEKVNMDODPKPALVTKEKENGSLSGLLQSCPPPLICR 119
DB 61 EVKAMNLKHEVLLLTSTENTLENDYVYGAALVTGEMENSLSGLLQSCPPPLICR 120
OY 120 LKEVYVGHFYLHNDQNPVLLHDLKPSNVLPDPPELVKADFLSTFGGSGSGSG-- 177
DB 121 LLEEVYVGHFYLHNDQNPVLLHDLKPSNVLPDPPELVKADFLSTFGGSGSGSG-- 180
OY 178 EPGGTGLYLAPELVFNVRKASTASDVYSPGILMNAVLAGEVELPTEPSLYEAVCNQ 237
DB 181 DSGGTGLYLAPELVFNVRKASTASDVYSPGILMNAVLAGEVELPTEPSLYEAVCNQ 239
OY 238 NRPSLAELOAGPEPFGELGKELKQLCMSSSEPKDRSPQECJPKTDEYFOVVENNMA 297
DB 240 NRPSLAELOAGPEPFGELGKELKQLCMSSSEPKDRSPQECJPKTDEYFOVVENNMA 299
OY 298 VSTVYKDFLSQKSSNRFSIPSGGGGTEMDGFRRTIENSHNDVYVSEMLNKLLEP 357
DB 300 VSKVYKYLQYRSSTKLKLSARRSSCKGTEVDCPRETI-----YEMLDRLHLEP 349
OY 358 PSSVPKCSLITRSRAQEQVPOAMTAGTSSDSMAOPPGTPTSTFRNOMSPSTGTP 417
DB 350 SGVPELSTLFR-NGKASRCHATPACTSSDTLACTPQIPHTLPSRGTTPRAPFTERP 408
OY 418 SPGRNOCAGKQNMNCRTERPVPYGRVLYNYSCVQVGNNTLTMOOTRLATPW 477
DB 409 GPDRKQGGGRNSNFWTWN-APNPTGLQSLVNLKSEVQIGQHNCVQPRKAPFK 467
OY 478 GLAPSGKRG 487
DB 468 EPAQFGRNG 477

RESULT 4
O96711 PRELIMINARY; PRT: 784 AA.
AC O96711;
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DE CDNA FLJ14518 FIS, CLONE NT2RM1000850, WEAKLY SIMILAR TO ANKYRIN R.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Isoqel T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
RA Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H.,
RA Nagatsuna M., Hosokita T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
RA Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi S.,
RA Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K.,
RA Yamamoto J., Wakamatsu A., Nakamura Y., Nagelharl K., Masuko Y.,
RA Minomura K., Iwayanagi T.;
RT "genomic DNA sequencing project."
RU Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AK027424; BAB5102.1;
SQ SEQUENCE 784 AA; 86348 MW; 05B193E84EB9E5AF CRC64;

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OY 59 --REKAMASLNEFVLRLEGVIEKVNMDODPKPALVTKEKENGSLSGLLQSCPPPL 116
DB 66 LIEBAKMEKAPRYILPYAGICRE-----PVGLWMEYMETGSLKELASE-PLPML 117
OY 117 LCRLKFEVYVGHFYLHNDQNPVLLHDLKPSNVLPDPPELVKADFLSTFGGSGSGSG 176
DB 118 RFRHHTAVGNMFLQMAPELLHDLKPSNVLPDPPELVKADFLSTFGGSGSGSGSG 177
OY 177 GEP-GGTGLYLAPELVFNVRKASTASDVYSPGILMNAVLAGEVELPTEPSLYEAV-C 234
DB 178 MDGFEIATLPELVFNVRKASTASDVYSPGILMNAVLAGEVELPTEPSLYEAV-C 236
OY 235 NRQRPSELAELOAGPEPFGELGKELKQLCMSSSEPKDRSPQECJPKTDEYFOVVENNMA 294
DB 237 VKGRPELPVPCARPR--ACSHLYRLNQRCMGCDPRVRPTFGETSETEDLCERPDDEV 294
OY 295 NAA-----VSTVYKDFLSQKSSNR-FRFSIPESGCGTEMDGFRRTIENSHNDVYVSE 348
DB 295 KETHADLVASPEPSEVYVPAKLRASAP-----TPNDYS-----LSL 335
OY 349 LKLN-----LEPP-----SVPAKCPSLTRSR-AQEQVPOAMTA-GTSSDSMAOP 396
DB 336 LQSDISVQAVDGPPELRSSEKSLPSGCRKLGSVDSVAFSSRGLSLSEFERP 395
OY 397 QTPETST 403
DB 396 STSDLGT 402

RESULT 5
O9H4D1 PRELIMINARY; PRT: 784 AA.
AC O9H4D1;
DT 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
DE 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE PROTEIN KINASE.
GN DTK.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE-20549657; PubMed-10948194;
RA Baehr C., Rohrer A., Stempke L., Rincke G., Marks F., Gschwendt M.;
RT "DTK, a novel protein kinase that interacts with protein kinase
RT Cdelta. Cloning, characterization, and gene analysis."
RU J. Biol. Chem. 275:36350-36357(2000).
DR EMBL: AJ278016; CAC04247.1;
DR HSSP; P25963; IINK.
DR InterPro: IPR002110; ANK.
DR InterPro: IPR000719; Euk_pkinase.
DR InterPro: IPR002390; Ser_thr_pkinase.
DR InterPro: IPR004040; STY_pkinase.
DR InterPro: IPR001245; Tyr_pkinase.
DR Pfam: PF00023; ank. 10.
DR Pfam: PF00069; pkinase. 1.
DR PRINTS: PR01415; ANKYRIN.
DR PRINTS: PR00109; TYRKINASE.
DR SMART: SM00248; ANK. 10.
DR SMART: SM00221; STYK. 1.
DR SMART: SM00220; S_TK. 1.
DR SMART: SM00219; TYRK. 1.
DR PROSITE: PSS0088; ANK_REPEAT. 9.
DR PROSITE: PSS0297; ANK_REPEAT. 1.
DR PROSITE: PSS0017; PROTEIN_KINASE_ATP. 1.
DR PROSITE: PSS0013; PROTEIN_KINASE_DOM. 1.
RW ANK repeat, ATP-binding; kinase; Repeat; Transferase.
SQ SEQUENCE 784 AA; 86407 MW; F3C7D5D2A35A9F1 CRC64;

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Query Match 14.5%; Score 401.5; DB 4; Length 784;

Best Local Similarity 30.0%, Pred. No. 8.3e-23;
Matches 128; Conservative 70; Mismatches 166; Indels 63; Gaps 16;

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OY 10 GAPAPLVISIE-----ELENOELVGRDGFVYFRAOHRKMGDYAVAVIVSKAIS----- 58
DB 6 GTPMALALIRTFDAGEFTGMEKVGSGGQYKVRHVHMKTMIAKCSPLHVDREHRE 65
OY 59 --REVANASLNEFVLREGYIEVENNDOPKALYTKFENKNGSLSGLLQSCPRPPL 116
DB 66 LLEAKKMKMAFRYILVYIGCRE-----PYGLVMEHMEGSLSEKLABE-PLPMDL 117
OY 117 LCRRLKEVYLGFIYLDONPVILHDLKPSNVLPDPLHKLADFGSLTFGGSGSGS 176
DB 118 RFRILHETAVAGNFIHCAAPPLHDLKPAVILDAHYHVKISDFGLACNGLSHSDLS 177
OY 177 GEP-GGTGLYLAPELVNVRKASTASDVYSGFILMAVLAGEVELPTESLYEAV-C 234
DB 178 MGLFETIYALPPEIRIREKSLRFDKHDVYSFALVIMGVLTQK--PFADEKNIILHMKV 236
OY 235 NNONRPSIALPQAGPERTGLEGLEKLMQCMSEPRKDRSPQECLPKDEVQVNEHNM 294
DB 237 VKGHRELPVVCARNR--ACSHLIRLMQRCMOGDPVRFTEITSETEDLCERPDDEV 294
OY 293 NAA-----VSTYKDFLSOLKSSN--RRFSIPSGGGGTMDGFRRTIENQSRNDVYSEW 348
DB 295 KETANDLVKSPPEPSEVVPARLKRASAP-----TEDNDYS-----LSEL 335
OY 349 LNKLN-----LEBP-----SSVPRKCPSLTKRSR--AQEQVQAMTA-GTSSDMAOP 396
DB 336 LSGLDGVSQAVGPELRSRSGSKLPSGSGKRLSGVSVDSAFSSRGLSLSFERE 395
OY 397 QTPETST 403
DB 396 STDGLT 402

RESULT 6
OY 096KHO PRELIMINARY: PRT: 784 AA.
AC 096KHO;
DB 01-DEC-2001 (TREMBLrel. 19, Created)
DB 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DB 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DB PROBABLE DUAL-SPECIFICITY SER/THR/TYR KINASE.
DB ANKRD3
DB Home sapiens (Human).
DB Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
DB Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
DB NCBI_TaxID=9606;
DB [1]
DB RP SEQUENCE FROM N.A.
DB RC TISSUE=FETAL KIDNEY AND FETAL LUNG;
DB RA Shimizu N., Kudoh J., Shiduya K.;
DB RT Homo sapiens mRNA for ANKRD3, complete cds.
DB RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
DB DR EMBL; AB047783; BAB56136.1;
DB KW KINASE.
DB SEQUENCE 784 AA; 86408 MW; F5E7DBD52A35A191 CRC64;

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Query Match 14.5%; Score 401.5; DB 4; Length 784;
Best Local Similarity 30.0%; Pred. No. 8.3e-23;
Matches 128; Conservative 70; Mismatches 166; Indels 63; Gaps 16;

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OY 10 GAPAPLVISIE-----ELENOELVGRDGFVYFRAOHRKMGDYAVAVIVSKAIS----- 58
DB 6 GTPMALALIRTFDAGEFTGMEKVGSGGQYKVRHVHMKTMIAKCSPLHVDREHRE 65
OY 59 --REVANASLNEFVLREGYIEVENNDOPKALYTKFENKNGSLSGLLQSCPRPPL 116
DB 66 LLEAKKMKMAFRYILVYIGCRE-----PYGLVMEHMEGSLSEKLABE-PLPMDL 117
OY 117 LCRRLKEVYLGFIYLDONPVILHDLKPSNVLPDPLHKLADFGSLTFGGSGSGS 176

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DB 118 RFRILHETAVAGNFIHCAAPPLHDLKPAVILDAHYHVKISDFGLACNGLSHSDLS 177
OY 177 GEP-GGTGLYLAPELVNVRKASTASDVYSGFILMAVLAGEVELPTESLYEAV-C 234
DB 178 MGLFETIYALPPEIRIREKSLRFDKHDVYSFALVIMGVLTQK--PFADEKNIILHMKV 236
OY 235 NNONRPSIALPQAGPERTGLEGLEKLMQCMSEPRKDRSPQECLPKDEVQVNEHNM 294
DB 237 VKGHRELPVVCARNR--ACSHLIRLMQRCMOGDPVRFTEITSETEDLCERPDDEV 294
OY 293 NAA-----VSTYKDFLSOLKSSN--RRFSIPSGGGGTMDGFRRTIENQSRNDVYSEW 348
DB 295 KETANDLVKSPPEPSEVVPARLKRASAP-----TEDNDYS-----LSEL 335
OY 349 LNKLN-----LEBP-----SSVPRKCPSLTKRSR--AQEQVQAMTA-GTSSDMAOP 396
DB 336 LSGLDGVSQAVGPELRSRSGSKLPSGSGKRLSGVSVDSAFSSRGLSLSFERE 395
OY 397 QTPETST 403
DB 396 STDGLT 402

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RESULT 7
OY 096KHO PRELIMINARY: PRT: 786 AA.
AC 096KHO;
DB 01-MAR-2001 (TREMBLrel. 16, Created)
DB 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DB 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DB PKC-REGULATED KINASE PKT.
DB ANKRD3.
DB Mus musculus (Mouse).
DB Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
DB Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
DB NCBI_TaxID=10090;
DB [1]
DB RP SEQUENCE FROM N.A.
DB RC STRAIN-BALB/C;
DB RX MEDLINE=2130307; PubMed=11278382;
DB RA Chen L., Halder K., Ponde M., Carlappa A., Roylitch D., Pillai S.;
DB "Protein kinase C-associated kinase (PKC), a novel membrane-
DB associated, Ankyrin Repeat-containing Protein Kinase.";
DB J. Biol. Chem. 276:21737-21744(2001).
DB EMBL; AF30127; AAG30871.1;
DB HSDP; P25963; IINK.
DB MSD; MGI:1919638; Ankrd3.
DB InterPro: IPR002110; Ank.
DB InterPro: IPR000719; Euk_Pkinase.
DB InterPro: IPR002290; Ser_Thr_Pkinase.
DB InterPro: IPR001245; Tyr_Pkinase.
DB Pfam; PF000023; ank; 10.
DB Pfam; PF00069; pkinase; 1.
DB PRINTS; PRO1415; ANKRIN.
DB PRINTS; PRO109; TYRKINASE.
DB SMART; SM00248; ANK; 10.
DB SMART; SM00221; STYK; 1.
DB SMART; SM00220; STYK; 1.
DB SMART; SM00219; TYRK; 1.
DB PROSITE; PS50088; ANK_REPEAT; 9.
DB PROSITE; PS50297; ANK_REPEAT_REGION; 1.
DB PROSITE; PS00107; PROTEIN_KINASE_DOM; 1.
DB ANK repeat; ATP-binding; Kinase; Repeat; Transferase.
DB KW ANK repeat; ATP-binding; Kinase; Repeat;
DB SEQUENCE 786 AA; 86702 MW; 8DB98977F5004787 CRC64;

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Query Match 14.4%; Score 399; DB 11; Length 786;
Best Local Similarity 30.3%; Pred. No. 1.3e-22;
Matches 127; Conservative 59; Mismatches 179; Indels 54; Gaps 13;

QY 20 ELENELVKTGDFGVFAQRKNGYDVAATYNSKAIS-----REVKAMASLDNEF 71
 DB 21 EFAGMEKVGSGGGVYVRRHVKHTWLAIKSPSLVNDREEMELLEAKKMEKAKFRY 80
 QY 72 VNLAESEVIEKVMDDPKPRALVTKFMENGSLGLOSCPRPILCLRLKEVLEMYL 131
 DB 81 ILPVYRIC-----QEP-VGLVMEWMEGSLKELKASE-PLPMDLFRIVHETAVNGMFL 132
 QY 132 HDONPVLRLDLPKSNVLPDELHVKLADPLSTFGGSGSGSGEPP-GGTGLYLAEL 190
 DB 133 HCHSPPLLDLPKSNVLPDELHVKLADPLSTFGGSGSGSGEPP-GGTGLYLAEL 192
 QY 191 FVNNKASTADYVTFGLIMAVLAGREVELPTEPSLYEAVCNQNPSTLAELPQAG 250
 DB 193 IREKSLPFDKIDVYSFAIVNGVLTQKKPPEADENKILHIMLVYVGRPELP--PICRP 250
 QY 251 EFTGLGLKELMQLCSEPPKDRSPFQCLPKTEDEVQVNNMNAVSTVDFLSOLKS 310
 DB 251 RPRACASLIGLMQRCHMDPQVRLPQETISSETDLCERKDE-----VNDLANE--- 300
 QY 311 SNRRFSIPSSGGGTEDMGFRRTIENHSHNDVNSMTKLNL-----LEPP-----SS 360
 DB 301 PGKSSLSLEKSSARPSSRLKASAPPD-NDCLSELSQLDSCISQTLGEPPELSRSS 359
 QY 361 VPKKPSLTKRRSAQEQVQAMTACTSSDSMAOPQTPETSTFRNQNSPTSTGPPSP 419
 DB 360 SECKLPSSSSGKR-----LSGVSYDNAFSSSGSLSTSFERE-----ASTDGLCP 404

RESULT 8
 ID 043353 PRELIMINARY; PRT; 540 AA.
 AC 043353;
 DT 01-JUN-1998 (TREMBLrel. 06, Created)
 DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE SERINE/THREONINE KINASE RICK (RECEPTOR-INTERACTING SERINE-THREONINE KINASE 2).
 GN RICK OR R1P2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN 1)
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98241596; PubMed=9575181;
 RA Inohara N., del Peso L., Koseki T., Chen S., Nunez G.;
 RT "Rick, a novel protein kinase containing a caspase recruitment domain,
 interacts with CLARP and regulates CD95-mediated apoptosis";
 RL J. Biol. Chem. 273:12296-12300(1998).
 RN 2)
 RP SEQUENCE FROM N.A.
 RX Ozerksy P., Holmes A., Broly M.;
 RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
 RN 13)
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98307936; PubMed=9642260;
 RA McCarthy J.V., Ni J., Dixit V.M.;
 RT "R1p2 is a novel NF-kappaB-activating and cell death-inducing
 kinase";
 RL J. Biol. Chem. 273:16968-16975(1998).
 RN 4)
 RP SEQUENCE FROM N.A.
 RX Thome M., Hofmann K., Burns K., Martillon F., Bodmer J.-L.,
 RA Maitman C., Tschopp J.;
 RT "Identification of CARDIAC, a RIP-like kinase that associates with
 caspase-1";
 RL Curr. Biol. 8:0-0(1998).
 RN 15)
 RP SEQUENCE FROM N.A.
 RX Blumberg P.M., Varon R.;
 RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
 RN 16)

RP SEQUENCE FROM N.A.
 RC TISSUE=SKIN, AND MELANOMA;
 RA Strausberg R.;
 RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 DR EMBL: AF027705; AAC34970.1; -;
 DR EMBL: AC004003; AAC24561.1; -;
 DR EMBL: AF028530; AAC27722.1; -;
 DR EMBL: AF064824; AAC25668.1; -;
 DR EMBL: AF117829; AAC04634.1; -;
 DR EMBL: BC004553; AAH04553.1; -;
 DR Interpro: IPR001315; CARD.
 DR Interpro: IPR000719; Euk_pkinase.
 DR Interpro: IPR002290; Ser_thr_pkinase.
 DR Pfam: PF00619; Kinase; 1.
 DR Pfam: PF00069; pkinase; 1.
 DR SMART: SM00114; CARD; 1.
 DR SMART: SM00221; STRC; 1.
 DR PROSITE: PS0209; CARD; 1.
 DR PROSITE: PS0011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
 KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferrase.
 SQ SEQUENCE 540 AA; 6194 MW; 575A692239505792 CRC64;

Query Match 13.7%; Score 379; DB 4; Length 540;
 Best Local Similarity 31.7%; Freq. No. 2.8e-21;
 Matches 101; Conservative 62; Mismatches 126; Indels 30; Gaps 11;

QY 14 PLVSEIELENQELVKGDFGVFAQRKNGYDVAATYNSKAISREVKAM 64
 DB 11 PTIPYHKLADLRILSGAGSGTSSARHADNRVQVAKHLIHPILDSEKDLREAEIL 70
 QY 65 ASDNEVRLAEVIEKVMDDPKPRALVTKFMENGSLGLOSCPRP---WPLLCRL 121
 DB 71 HKAFFSIILPILGICNEPPE-----LGIVTEYMPGSLNELKRTETPDVAMPRLFRIL 125
 QY 122 KEYVLFYLDONPVLLRLDLPKSNVLPDELHVKLADPLSTFG- GSGSGSGSGEPP 179
 DB 126 HEIADLVNVTNNHTPPLHLDLKTQNLILDNHFKIADPLGSLKRNRMGSLSSRSRSKAP 185
 QY 180 -GGTGLYLAELF-VVNNKASTADYVTFGLIMAVLAGRE-VELPTEPSLYEAVCNR 236
 DB 186 EGGIIVMPENEPQKSRASIKHDIYSAVITWEVLSKRPEDVTNPDIQIMYSV-SQ 244
 QY 237 QNRSLAE--LPQAGETGLEGLELMQLCSEPPKDRSPFQCLPKTEDEVQVNN- N 292
 DB 245 GHRVYNESLPY--DIPHRARMTSLIESGMQNPDRSPFLKLELPVLRFEET 301
 QY 293 NMNAAVSTVDFLSOLKS 311
 DB 302 FLKAVIOIKTKLQSVSSA 320

RESULT 9
 ID 09B125 PRELIMINARY; PRT; 527 AA.
 AC 09B125;
 DT 01-JUN-2001 (TREMBLrel. 17, Created)
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE SHK1 PROTEIN.
 GN SHK1.
 OS Dictyostellium discoideum (Slime mold).
 OC Eukaryota; Mycetozoa; Dictyostellidae; Dictyostellium.
 OX NCBI_TaxID=44689;
 RN 1)
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21172738; PubMed=11274054;
 RA Montaliis J.;
 RT "An SH2-domain containing kinase is a negative regulator of the
 phosphatidylinositol-3 kinase pathway";

RL Genes Dev. 15:687-698(2001).
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 DR EMBL: AJ297966; CAC35360.1.
 DR HSSP: P08631; 1AD5.
 DR InterPro: IPR000719; Euk-kinase.
 DR InterPro: IPR002290; Ser-thr-kinase.
 DR InterPro: IPR000980; SH.
 DR InterPro: IPR001245; Tyr-kinase.
 DR Pfam: PF00069; tyrosinase.
 DR PRINTS: PR00109; tyrosinase.
 DR SMART: SM00252; SH2.1.
 DR SMART: SM00220; SH2.1.
 DR SMART: SM00219; Tyrc: 1.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; UNKNOWN_1.
 DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE: PS50108; PROTEIN_KINASE_ST; 1.
 DR PROSITE: PS50001; SH2.1.
 DR ATP-binding: Serine/threonine-protein kinase; transferase.
 KW SEQUENCE 527 AA; 59505 MW; 19876B03B78F98E CRC64;

Query Match 12.3%; Score 340; DB 5; Length 527;
 Best Local Similarity 28.5%; Pred. No. 3e-18;
 Matches 128; Conservative 69; Mismatches 154; Indels 98; Gaps 23;

QY 14 PLVSIELNDELNGKDGCGTFRPAQHRKRGYDAVKI-----VNSKAIIS---REYKAMAS 66
 DB 38 PELSETETTESITLGGSGFGYVYKGRCL--KDPVAVMLKQVDKTLDFRREVALNSK 95
 QY 67 LDNEFYLRLEGVIEVNMDDPRPALVTKFMENGSLSGLLQSCPPRPPLCRLLKEVYL 126
 DB 96 IFRPNVLTGLACTST-----PKMLICETELKGNLESLLDPMVKLPYLTRMMADAL 151
 QY 127 GMFYLTIDQNPVLHRLDKPSNVLPPELHVKLADFGISTE--GGSSGSGSGSGEGGTG 185
 DB 152 GYVLMHSSNPVPIHNDLTKSNLYDANLYVAVCFGLSQKQKQENLKQDQCAKSTPLM 211
 QY 186 LAPELFEVN--VNRKASTASDVYSGITLMAVLAEREVELTEPSL--VTEAVCNRRPS 241
 DB 212 MAEYVLOGRLFEKKA---DVSFGLVLMQFTREQEL--FEFNFNFRFAALCEKOLRPS 266
 QY 242 LAELPACGETPGLGLKELMLQKLSSEPKRPSFOR-----CLPKTDEVFM 289
 DB 267 ---IPDCKRS-----LRELICKMDPRPEVRPSEFIVSLEELIIDCIP--DEYGA 316
 QY 290 V-----ENNMAAVSVTKIDLS-----QLKSSNRFSIPESGOGGTENMGFRRTIE- 335
 DB 317 LKRNHRKHNENAN-----WKDTNVSFNVGLTNANRP--SKSDLDQSPPLMG--STIEL 368
 QY 336 -----NOHSRNDVMSSEMLNKL---NLEPPSSVPRKCPSLTKRSRAQEE 377
 DB 369 NFKCLSIIVSPKGPHEEVLVLMQFCKVLAMFGNLKEDGSOILDKIRQL----- 419
 QY 378 QVPOAWTAG--TSSDSMAOPROTPESTFE 404
 DB 420 -MECAWFHGDISTSESENLRQKRP-GTF 446

RESULT 10
 Q9SR87 PRELIMINARY; PRT; 693 AA.
 AC Q9SR87; 01-MAY-2000 (TREMBLrel. 13; Created)
 DT 01-MAY-2000 (TREMBLrel. 13; Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19; Last annotation update)
 DE PUTATIVE SERINE/THREONINE PROTEIN KINASE.
 GN T16011.20.
 OS Arabidopsis thaliana (mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC Eucosids II; Brassicales; Brassicaceae; Arabidopsiis.
 OC NCBI_Taxid-3702;
 RN [1]

RP SEQUENCE FROM N.A.
 RC STRAIN-CV, COLUMBIA;
 RA Lin X., Kaul S., Town C.D., Benito M., Creasy T.H., Haas B.,
 RA Bonnin C.M., Koo H., Fujii C.Y., Utterback T.R., Barnstead M.E.,
 RA Bowman C.L., White O., Nierman W.C., Fritch C.M.,
 RT Arabidopsis thaliana chromosome III BAC T16011 genomic sequence.*;
 RL Submitted (JAN-2001) to the EMBL/GenBank/DBS databases.
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 DR EMBL: AJ30871; BAF07845.1.
 DR HSSP: P13306; ILDE.
 DR InterPro: IPR000719; Euk-kinase.
 DR InterPro: IPR001220; Lectin_1egB.
 DR InterPro: IPR002290; Ser-thr-kinase.
 DR InterPro: IPR004040; STY-kinase.
 DR Pfam: PF00139; Lectin_1egB; 1.
 DR Pfam: PF00069; tyrosinase.
 DR SMART: SM00211; STYK; 1.
 DR PROSITE: PS50107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE: PS50108; PROTEIN_KINASE_ST; 1.
 KW ATP-binding; kinase; Serine/threonine-protein kinase; transferase.
 SO SEQUENCE 693 AA; 77600 MW; 0EDBDA0303D5DE4 CRC64;

Query Match 12.0%; Score 333; DB 10; Length 693;
 Best Local Similarity 30.5%; Pred. No. 1.6e-17;
 Matches 101; Conservative 71; Mismatches 115; Indels 44; Gaps 15;

QY 16 VSIELENOELNGKDGCGTFRPAQHRKRGYDAVKI-----REVKAMASLDN 69
 DB 363 LATKFESEIIIGTGFGIVYNGNLSGSG--PIAVKTKTSLSLGGVREFMAITESIGRLGH 421
 QY 70 EFVLRLEGVIEKVMDDPRPALVTKFMENGSLSGLLQSCPPRPPLCRLLKE 123
 DB 422 KNIVNAGCKKHN-----ELLITDYIPNGLSDSLY--QFRRNGIYLPVDVFEIIG 475
 QY 124 VYDAMFTLHQ--NPVLHRLDKPSNVLPPELHVKLADFGIS--TGGSSGSGTSGSGPG 181
 DB 476 IASGLTLHEMVDQIVHNDVPSVLTIDEDNNAKLGDELARLEKTL--TOTYIIG 533
 QY 182 TLGYLAPELFEVNVRKASTASDVYSGITLMAVLAEREVELTEPSLYEA--VCNRON 238
 DB 534 TLGYMAEL--FANGSGTASDVAFAGVLLLEIVCNRK---PTNENFFLDVMEHRTN 588
 QY 239 RPSLAELPO-AGEETPGLGLKELM--QICHSEPPDRPSF-----OELPKTDEV 286
 DB 589 GGLICVYDQNLSSFRKREARIALVGLLCHORPKFRPSNMWTLRIYNGSENVPOIDEN 648
 QY 287 FQVYENNNNAVSVTKIDLSQK--SSNRPS 316
 DB 649 WGFSDSRDDHRSNVVGVYSSDRASSSTPS 679

RESULT 11
 Q9H1Y7 PRELIMINARY; PRT; 564 AA.
 AC Q9H1Y7; 01-MAR-2001 (TREMBLrel. 16; Created)
 DT 01-MAR-2001 (TREMBLrel. 16; Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19; Last annotation update)
 DE D1662P8.3 (SIMILAR TO NAF310 (MITOGEN-ACTIVATED PROTEIN KINASE KINASE KINASE 10)) (FRAGMENT).
 GN D1662P8.3.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OC NCBI_Taxid-9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Hall R.;
 RL Submitted (MAY-2000) to the EMBL/GenBank/DBS databases.
 DR EMBL: AL33380; CAC17571.1;
 DR HSSP: P06241; 1SHF.

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DR InterPro: IPR000719; Euk_pkinase.
DR InterPro: IPR002290; Ser_thr_pkinase.
DR InterPro: IPR001452; SH3.
DR InterPro: IPR001245; Tyr_pkinase.
DR Pfam: PF00069; pkinase; 1.
DR Pfam: PF00018; SH3; 1.
DR PRINTS: PR00452; SH3DOMAIN.
DR PRINTS: PR00109; TYRKINASE.
DR SMART: SM00326; SH3; 1.
DR SMART: SM00220; S_TKC; 1.
DR SMART: SM00219; TYKC; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS50002; SH3; 1.
DR ATP-binding; Kinase; Transferase.
FW NON_TER 564 564
SQ SEQUENCE 564 AA; 62400 MW; DAFL9LE14842E7EB CRC64;

Query Match 11.7%; Score 324.5; DB 4; Length 564;
Best Local Similarity 26.5%; Pred. No. 5.4e-17;
Matches 130; Conservative 70; Mismatches 185; Indels 103; Gaps 21;

OY 8 PSCGAP-----LVSEELNEQELVGRGEGTFVRAOHRM-GYDAVAVIV----- 53
DB 102 PAASPAAPPSPSPVHVAFERLELEKELIGAGFGGYRA---TWQGEVAVAAKADPE 158
OY 54 -----SKAIREVKMAASLDNEFVLRLEVEKVNMDQPKALVYTKFKENGSLGLQ 107
DB 159 QDAALAAEVRRAFLFPAHLRPNITELRGCL-----QPHCLVLEFRGALRALA 213
OY 108 SOCPRPWP-----LICRLKEVYLCMFYLDONPV-LLRDLKPSNVLDP 152
DB 214 AANAADPPRAPGRARRIRPVLVMAVQALRGMLLHEBAVLPILHDLKSSNILL 273
OY 153 ELH-----VLADFGSLSTFGSGSGSGSGPGLTGLAPELFVNNKRASTADY 204
DB 274 KIEHDICNKTJKTIDFGLAR---EMHRTIKMSTAGTYAMAPV-VIKSLFSGSDI 327
OY 205 YSGGILMAVLAAGREVELTER---SLVYAVCNRRNRSLAELOAGPEPGLGLEKE 260
DB 328 WSTGVGLMELTGS---EYVYRGIDGLAVAVVANKTLTP---IPSTPEP---PAK 375
OY 261 LMDLCSSEPKDRPSFOECLPR-----TDEPVQVNNNAVAVSTVKDFL--- 305
DB 376 LMECHQODPHIRSFALILEQALIECAVNTKMPQSFHSDMKLEIQMFDELARK 435
OY 306 -SOLKSNRRFSIPESGCGCTEMDGFRTINQHSRDVAVSEKN-----KMLEPPSS 360
DB 436 EKELRSREELTAALQSQEELKREQLAREIDVLERE-LNLILOLMOEKPK-- 492
OY 361 VPKCPSLTKRSRAOEVOYPOAMTAGTSSD-----SMAOPQTPETSTERNQSPSTG 415
DB 493 -VKKRKGKFKRSRL---KIKDGHRIPLSDQHKITQVQASPNDKRRSLNSSSSPSPSS 548
OY 416 TSPGPGRNO 425
DB 549 TNPRLRAIQ 558

RESULT 12
OY0307 PRELIMINARY; PRT; 667 AA.
AC OY0307;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE RECEPTOR-LIKE PROTEIN KINASE.
GN F18N11.180.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eustosids II; Brassicales; Brassicaceae; Arabidopsis.

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OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Jordan N., Bangert S., Wiedemann R., Voss H., Unsel N., Mewes H.W.,
RA Lemcke K., Mayer R.F.X., Queller F., Salanoubat M.;
RL Submitted (NOV-1999) to the EMBL/Genbank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA EU Arabidopsis sequencing project;
RL Submitted (FEB-2000) to the EMBL/Genbank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL: AL132933; CAB72491.1; -.
DR HSSP: P02870; ILEN.
DR InterPro: IPR000719; Euk_pkinase.
DR InterPro: IPR001220; Lectin_legB.
DR InterPro: IPR002290; Ser_thr_pkinase.
DR InterPro: IPR004040; STY_pkinase.
DR InterPro: IPR001245; Tyr_pkinase.
DR Pfam: PF00139; Lectin_legB; 1.
DR Pfam: PF00069; pkinase; 1.
DR PRINTS: PR00109; TYRKINASE.
DR SMART: SM00221; STYKC; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS50108; PROTEIN_KINASE_ST; 1.
DR ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 667 AA; 74097 MW; 65F2P83FD4A26DBF CRC64;

Query Match 11.6%; Score 321.5; DB 10; Length 667;
Best Local Similarity 32.5%; Pred. No. 1.2e-16;
Matches 103; Conservative 48; Mismatches 113; Indels 53; Gaps 14;

OY 26 LVGDGEGTFVRAOHRMGYDAVAVIV-----SKAIREVKMAASLDNEFVLRLEGYI 79
DB 355 LVGGGEGGKYYKGF-LPGGRHIAVKRLSHDAQGKQFVAEYVTNGNIQRNLYVPLGYC 413
OY 80 EKVNNDDPPRALVYTFMENGSLG-LLOSOPRP-NPLICRLKEVYLCMFYLDONP 136
DB 414 RRGK-----ELLVSEYKNGSLDQYLFYQNPSPSWLQRIILKDIASLNTLHSGANP 468
OY 137 VLHRDLKPSNVLDPPELHVKLADFGSLSTFG--GSGSGTSGSGEGTGLAYLAPELFVNV 194
DB 469 AVLHRDIKASVMDSEYNGRLDDEGMKAFQDPQGNLSATPA---VGTIYMAPEL---I 522
OY 195 NRKASTADYVSGGILMAVLAIGR---EVELPTPESLVYEAVCNRRNPSELAEI--PQAG 249
DB 523 RTGSKETDVTYAGTIFLVEYTCGRPFEPZELPVQKTIYKVCCHQASLLETBDPKIG 582
OY 250 PE--TPGLGKLEMDLCSSEPKDRPSFOECLPRIDEVQVNNNAVAVSTVKDFLSQ 307
DB 583 REFLSEVEVNLKIGLCTNDVPSRPD-----NGOVMOYLSQ 620
OY 308 LKSNRRFSIPESGCG 324
DB 621 -KQPLPDPFSADSPGIG 636

RESULT 13
OY0420 PRELIMINARY; PRT; 688 AA.
AC OY0420;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE RECEPTOR LIKE PROTEIN KINASE.
GN F7A7.70.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eustosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]

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RP SEQUENCE FROM N.A.
 RA Beyer M., Pohl T., Weizenegger T., Bancroft I., Neues H.W., Rudd S.,
 RA Lemcke K., Mayer K.F.X.: the EMBL/GenBank/DBJ databases.
 RL Submitted (Mar-2000) to the EMBL/GenBank/DBJ databases.
 RN (2)
 RP SEQUENCE FROM N.A.
 RA EU Arabidopsis sequencing project;
 RL Submitted (Mar-2000) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 DR EMBL: AL161946; CAB8227.1; -
 DR HSSP: P16404; 1A27.
 DR Interpro: IPR000719; Euk_pkinase.
 DR Interpro: IPR001220; Lectin_legb.
 DR Interpro: IPR002280; Ser_thr_pkinase.
 DR Interpro: IPR004040; STY_pkinase.
 DR Interpro: IPR001245; Tyr_pkinase.
 DR Pfam: PF00139; Lectin_legb; 1.
 DR Pfam: PF00069; pkinase; 1.
 DR PRINTS: PR00109; TYRKINASE.
 DR SMART: SM00221; STYKC; 1.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE: PS00111; PROTEIN_KINASE_DOM; 1.
 DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
 DR ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
 KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
 SQ SEQUENCE 688 AA; 73984 MW; DDAFPA68947EC3 CRC64;

Query Match 11.6%; Score 320.5; DB 10; Length 688;
 Best local similarity 31.4%; Pred. No. 1,3e-16;

Matches 101; Conservative 66; Mismatches 118; Indels 37; Gaps 15;

DB 22 ENDELGKGFVTFRAQHRKGYD-VAVKYNKSAISRETKMASIDNEFVLRGCVTE 80
 ||:|||||
 DB 363 ENR-IVCTGCTGCTVFGNLSPPSSDQIAVKITRPSMCGVREFAEESAGRLRHKNLVN 421
 ||:|||||
 DB 81 KVMV-DQDRPALVYTKENSGSLGLOSQCPR-----PAPLCRLLEEVYLGMYLND 133
 ||:|||||
 DB 422 LQCMCKQKNDLLIYDIPNGSLDLSLYSR-PROSGVTLNNAFKXAKIASGLIYTHE 480
 ||:|||||
 DB 134 Q-NPVLHRLDKPSNVLPPPELHVLAIDFGLS-TFOGSGSGTSGEGCGTGLYLAPELF 191
 ||:|||||
 DB 481 EMKCVIYHDIKPSNVLIEDDMNRLGDFGLARLYERGOSQNT--TVVGTCTGYMAPEL- 537
 ||:|||||
 DB 192 VVNVRRASADVSFGICLMAVLAEREVELTEPESLYEKA--VCNRNRPRL--AELNQ 247
 ||:|||||
 DB 538 -ARNGSSASADVFAPAGVLLLEIYSGNR--PTDSGTFILADVMELAHAGETLHAVDPR 593
 ||:|||||
 DB 248 AGEPTGLEGLKELM--OLCMSSEPKDRPSQECI-----PKTDEVFQWVENNNNA 296
 ||:|||||
 DB 594 LGFGYGVGEARLALVGLLCCHQRPTRSPSRVRLRYLNGDDVDVPEIDNDMGVSDSSRD 653
 ||:|||||
 DB 397 AVSTVDFPDLQSKSSNRPSIP 318
 ||:|||||
 DB 654 LGSNFGYVSDRASS---SVF 672
 ||:|||||

RESULT 14
 ID 09N270 PRELIMINARY; PRT; 491 AA.
 AC 09N270;
 DT 01-OCT-2000 (Tremblrel. 15, Created)
 DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
 DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
 DE TGF BETA-ACTIVATED KINASE SPLICED VARIANT D.
 GN TAK1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN (1)
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20368765; PubMed=1118615;
 Dempsey C.E., Sakurai H., Sugita T., Guesdon F.;

RT *Alternative splicing and gene structure of the transforming growth
 RT factor beta-activated kinase 1".
 RL Blochum. Biophys. Acta 1517:46-52(2000).
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 DR EMBL: AF218074; AAF27652.1; -
 DR HSSP: P08631; 1AD5.
 DR Interpro: IPR000719; Euk_pkinase.
 DR Interpro: IPR002290; Ser_thr_pkinase.
 DR Interpro: IPR004040; STY_pkinase.
 DR Interpro: IPR001245; Tyr_pkinase.
 DR Pfam: PF00069; pkinase; 1.
 DR PRINTS: PR00109; TYRKINASE.
 DR SMART: SM00221; STYKC; 1.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE: PS00111; PROTEIN_KINASE_DOM; 1.
 DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
 DR ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
 KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
 SQ SEQUENCE 491 AA; 53739 MW; B7D8832E286A99C5 CRC64;

Query Match 11.5%; Score 318.5; DB 4; Length 491;
 Best local similarity 25.7%; Pred. No. 1,3e-16;

Matches 129; Conservative 74; Mismatches 165; Indels 133; Gaps 25;

DB 11 APAPVSTIE-----ELENELGKDGCTVFRQAHRW-GYDAVATVNS---KAISRE 60
 ||:|||||
 DB 21 APSQVLFNEEDIDYKEIEVEEYVGRGAFGVCKA---KMRKADVAIQISESEERAFIVE 77
 ||:|||||
 DB 61 VKAASLDNFEVLRLEGV-IEKYNDDOPKRALYTKFNENSGSLGLOSQCPR----- 113
 ||:|||||
 DB 78 LRQSLRVNHPNIVKLGACLNPNV-----CLMVEYAEGLSYLVNLAHCARPLPYTAAH 129
 ||:|||||
 DB 114 ---PPLCRLLEEVYLGMYLNDQNP-VLHRLDKPSN-VLPPPELHVLAIDG-----LS 164
 ||:|||||
 DB 130 AMSKGLDGS-----OGAVILSHQPKALIHRLDKPPLLVAGGVTLVLCDFGACDIO 183
 ||:|||||
 DB 165 TFOGSGSGTSGEGGTGLYLAPELFVNVNRKASTADYSGCILMNAVLAGREV--EL 222
 ||:|||||
 DB 184 THMTNNK-----GSAAMNAPVDFGSGN--YSEKCDVFSWGIILMVTIRRRPDEI 232
 ||:|||||
 DB 223 PTEPSLYEAVCNORNPRLAELPOAGPETGLEGLKELQ/LCMSSEPKDRPSQECI-- 280
 ||:|||||
 DB 233 CGPAPRIMNAVHNGTNPRLIKLPPK-----IESLWTRCMSMDPQRSMEIYKI 283
 ||:|||||
 DB 281 -----PTDEVQNV-----ENMNAVSTYKVDPLSOLKSNRPSIPSSGGCGTEM 327
 ||:|||||
 DB 284 MTHLMRYFPGADEPLDLPQOYSDGQSNAST-----GSEW 320
 ||:|||||
 DB 338 DGFRTIENQSHNDVAVSEMLKILEEPPSS--VPKCPSLTKRSRAQEDVQAWTA 385
 ||:|||||
 DB 331 D-----IASNTSNK-----SDTNMEQVATNDTIKRLSKLKNQAKQSGESGRSL 368
 ||:|||||
 DB 366 GTSDSMAQP-PQTPETSTFRNOPS-----PTSTGTPSPGPGNGCAROGMNSCHTP 439
 ||:|||||
 DB 369 GASRSSVESLPLTSSKKKMSADNSIEARLAATGNGQPRRSIDQLTVTQ-----T 421
 ||:|||||

RESULT 15
 ID 093YUO PRELIMINARY; PRT; 765 AA.
 AC 093YUO;
 DT 01-DEC-2001 (Tremblrel. 19, Created)
 DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
 DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
 DE HYPOPHYSICAL 85.1 KDA PROTEIN.
 GN ATIG67890.
 OS Arabidopsis thaliana (mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;

OC eucroide II; Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Yamada K., Banh J., Banno F., Chang E., Dale J.M., Goldsmith A.D.,
 RA Lee J.M., Onodera C.S., Quach H.L., Tang C., Toriumi M., Wu H.C.,
 RA Yamamura Y., Yu G., Yu S., Bowser L., Carriacci P., Chen H., Cheuk R.,
 RA Hayashizaki Y., Ishida J., Jones T., Kamiya A., Karlin-Neumann G.,
 RA Kawai J., Kim C., Koeseema E., Lam B., Lin J., Meyers M.C., Miranda M.,
 RA Narusaka M., Nguyen M., Palm C.O., Sakurai T., Satou M., Seki M.,
 RA Shinn P., Southwick A., Tracy S.E., Shinozaki K., Davis R.W.,
 RA Ecker J.R., Theologis A.;
 RT *Full Length cDNA of gene At1g67890 (GI:15220577).
 RL Submitted (Oct-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY059769; AAL24117.1;
 KM Hypothetical protein.
 SQ SEQUENCE 765 AA; 65149 MW; 6651738FBAE347D4 CRC64;

Query Match 11.5%; Score 318.5; DB 10; Length 765;
 Best Local Similarity 34.4%; Pred. No. 2,4e-16;
 Matches 98; Conservative 41; Mismatches 101; Indels 45; Gaps 11;
 QY 19 EELNQLVKGDKGFGTVFRAQHRK-GYDAVKIKNSKAIS-----REVKAMASLDN 69
 Db 485 EDLTNGEIQGGSCGTV---HGLMFGSDVAVKVSKEVSEETISFKQVSLMKRLRH 541
 QY 70 EFLRLKECVIEKVMNDQPKRALVTKPMENSLSGLIQ-SQCPRPPLCLRLKEVYLGM 128
 Db 542 PNVLFMGAVA-----SPQRLCTVTEFLPQSLFRLQNNKSKLDLRRIHNASDIARGM 596
 QY 129 FYLADQNPVLLHRDLKPSNVLPPELHVKLADFGQLSTFGGSGSGTSGSGEGTLAGYLAP 188
 Db 597 NYLHRCSPPIIHRDLKSSNLLVDRMWTYKADFGLSRKHETVLTNG--RGTPQWMAP 653
 QY 189 ELFVNVRKASTASDVYSFGILMAVAVLAGREVELTEPSLVYEAVCNCRQNPRLAELPQA 248
 Db 654 E--VLNENADEKSDVYSQVYLM-----ELVTE-KIPWE-----NLNAQVIGAV 696
 QY 249 GPTPTGLEKLE-----LMQLCMSSEPRDRPSFOCLPKTDEY 286
 Db 697 GPNQRLEVPKDVDPQWITALMESCWHSEPCQRPSPFOELNDKREL 741

Search completed: August 13, 2002, 22:14:15
 Job time: 462 sec

GenCore version 4.5
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OM protein - protein search, using 6w model

Run on: August 13, 2002, 22:08:18 ; Search time 24.11 Seconds
(without alignments)
833.490 Million cell updates/sec

Title: US-09-762-491-6
Perfect score: 2774
Sequence: 1 MSCKLWPSGAPAPLVISE.....PRDPEANSRPGCWYNSGRZ 519

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database: SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	445.5	16.1	656	1 RIP_MOUSE	Q06855 mus musculu
2	423	15.2	671	1 RIP_MOUSE	Q13346 homo sapien
3	401	14.5	832	1 ANR3_HUMAN	P57078 homo sapien
4	321	11.6	606	1 M3K7_HUMAN	O43118 homo sapien
5	312.5	11.3	579	1 M3K7_MOUSE	O62073 mus musculu
6	303	10.9	954	1 M3KA_HUMAN	O02779 homo sapien
7	302	10.9	821	1 CTR1_ARATH	O05609 arabidopsis
8	295.5	10.7	628	1 TESK_RAT	O63572 rattus norv
9	294.5	10.6	513	1 AVR2_SHEEP	O28660 ovis aries
10	292.5	10.5	513	1 AVR2_RAT	P38644 rattus norv
11	290.5	10.5	513	1 AVR2_BOVIN	O28043 bos taurus
12	290.5	10.5	513	1 AVR2_HUMAN	P27037 homo sapien
13	290.5	10.5	513	1 AVR2_MOUSE	P27038 mus musculu
14	287.5	10.4	394	1 M3K9_HUMAN	P80192 homo sapien
15	286.5	10.3	514	1 EPBR_XENLA	P27039 xenopus lae
16	286.5	10.3	902	1 EPBR_XENLA	P54762 xenopus lae
17	285.5	10.3	984	1 EPB1_HUMAN	O91735 kenopus lae
18	285.5	10.3	984	1 EPB1_RAT	O91735 kenopus lae
19	285	10.3	974	1 EPB3_XENLA	O70405 mus musculu
20	283	10.2	1051	1 URK1_MOUSE	O70405 mus musculu
21	282	10.2	976	1 EPB2_HUMAN	P23117 homo sapien
22	281	10.1	888	1 M3KC_MOUSE	O60700 mus musculu
23	279.5	10.1	984	1 EPB1_CHICK	O07494 gallus gall
24	276.5	10.0	501	1 KPEL_DROME	O05652 drosophila
25	276.5	10.0	512	1 AVR8_BOVIN	O95126 bos taurus
26	276.5	10.0	512	1 AVR8_HUMAN	O13705 homo sapien
27	276	9.9	901	1 CR14_MAZE	O24585 zea mays (m
28	276	9.9	1004	1 EPB2_CHICK	P26993 gallus gall
29	275.5	9.9	926	1 EPB1_HUMAN	P21709 homo sapien
30	275	9.9	888	1 M3KC_RAT	O63196 rattus norv
31	273	9.9	977	1 EPB2_MOUSE	O03145 mus musculu
32	273.5	9.9	1055	1 EPB2_HUMAN	P29323 homo sapien
33	273.5	9.9	981	1 EPB3_HUMAN	O13146 brachydanio

34	273	9.8	987	1 EPB2_COTJA	O90344 coturnix co
35	273	9.8	1308	1 EPB4_HUMAN	O15303 homo sapien
36	272.5	9.8	536	1 AVR8_MOUSE	P27040 mus musculu
37	272.5	9.8	1520	1 ABL_DROME	P00522 drosophila
38	272	9.8	746	1 ABL_HUMAN	P00521 abelson mur
39	272	9.8	993	1 EPB2_MOUSE	P54763 mus musculu
40	271.5	9.8	354	1 KHOS_MSVMT	P32593 moloney mur
41	271.5	9.8	374	1 KHOS_MSVMO	P00538 moloney mur
42	270.5	9.8	630	1 TBC_MOUSE	P24604 mus musculu
43	270.5	9.8	1002	1 EPB5_CHICK	O07497 gallus gall
44	270	9.7	382	1 AVR8_RAT	P38445 rattus norv
45	270	9.7	859	1 M3KC_HUMAN	O12852 homo sapien

ALIGNMENTS

RESULT 1
RIP_MOUSE STANDARD: PRT; 656 AA.
ID RIP_MOUSE
AC Q60855;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Serine/threonine protein kinase RIP (EC 2.7.1.-) (Cell death protein
DE RIP) (Receptor interacting protein).
GN RIP1 OR RIP OR RIMP.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid:10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-C57BL/6 X CBA; TISSUE-Thymus;
RX MEDLINE-95277838; PubMed-7538908;
RA Stanger B.Z., Leder P., Lee T.-H., Kim B., Seed B.;
RT "Rip: a novel protein containing a death domain that interacts with
RT Fas/Apo-1 (CD95) in yeast and causes cell death.";
RL Cell 81:513-523(1995).
CC -1- FUNCTION: INTERACTS WITH THE DEATH DOMAIN OF FAS AND TRADD AND
CC INITIATES APOPTOSIS. IT IS RECRUITED BY TRADD TO TNFRI IN A TNF-
CC DEPENDENT PROCESS. REQUIRED FOR TNFRI ACTIVATION OF NF-KAPPA B.
CC -1- TISSUE SPECIFICITY: FOUND AT LOW LEVELS IN ALL TISSUES.
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC -1- SIMILARITY: CONTAINS 1 DEATH DOMAIN.
CC -----
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CC -----
CC EMBL: U25995; AAB60487.1; -
CC HSSP: P13362; JAGW.
DR MGD: MGI:108212; RRP1.
DR InterPro: IPR000488; Death.
DR InterPro: IPR000719; Euk_kinase.
DR InterPro: IPR004040; STY_kinase.
DR InterPro: IPR002290; Ser_thr_kinase.
DR Pfam: PF00531; death.1.
DR Pfam: PF00069; pkinase.1.
DR SMART: SM00005; DEATH; 1.
DR SMART: SM00221; STYK; 1.
DR PROSITE: PS00108; PROTEIN KINASE ST; 1.
DR PROSITE: PS50011; PROTEIN KINASE DOM; 1.
DR PROSITE: PS50017; DEATH_DOMAIN; 1.
KN Transferrase: Serine/threonine-protein kinase: ATP-binding;
KM Apoptosis.
FT DOMAIN 17 290 PROTEIN KINASE.
FT NP_BIND 23 31 ATP (BY SIMILARITY).
FT BINDING 49 49 ATP (BY SIMILARITY).
FT

FT ACT_SITE 138 138 BY SIMILARITY.
 FT DOMAIN 568 654 DEATH.
 FT VARIANT 473 473 T->I.
 SQ SEQUENCE 656 AA: 74854 MW: ABB350B23879933 CRC64:

Query Match 16.1%; Score 445.5; DB 1; Length 656;
 Best Local Similarity 26.2%; Pred. No. 2.6e-20;
 Matches 158; Conservative 89; Mismatches 205; Indels 151; Gaps 23;

QY 15 LVSELENGEVLGKDGSTVFRAGHRKMGDVAVKIVN-----SKASREYKMAST 67
 DB 12 MASSDLEETDL-DSGGGRKVSICFHRSHGVYIAKKTGTGNGRAETINEVLEEGKMMRL 70
 QY 68 DNEFVRLSEGVIEKVMQDQKRALVYKFMENGLSGLLQSCPPRPMLLCRLKEVYL 126
 DB 71 RHRVVKLLGIIIEEGVY-----SLVMEYKMGKLNHVKLTQIDVPLSKRHIIVEAE 124
 QY 127 GNFYLDQNPVLLHRLDKPSNVLPPPELVKRLADFGSLTFQSGSO-----SGT 174
 DB 125 GNCYLHDKG--VIHDKLRKENTLVDRDFHRIKADLVASRTSKLTKKMDKOKEVST 182
 QY 175 GSGEPGCTGLYLAPELVFNVRNKAASADYVSGCLMAYLAGREVELPTREPLVLAAC 234
 DB 183 TKRNGSGTLYMAPPELMDINKPTKSDVSGFVLMALFAKKE--PYE-----NVIC 234
 QY 235 NMQ-----NPSLAELPQAGPETPGLKELMQLCMSSEPKDRPSP---QDECLPK 282
 DB 235 TEEFVVICIKSNRPVNEETIEECPRE-----IISLMERCQALPEDEPFLGIEEFPRF 289
 QY 283 TDEVF--QVENVNMANAVSTVNDFLSKLSNRFS-----TPES----- 320
 DB 290 YLSHFEEVYEEDEV---ASLAKKETPQSPVYLQRMFSLQHDVCLPSPSSNSEQSGLSHSG 346
 QY 321 --CGGCTEMDCFRRTLEQNSHNDVMSYENK-----LNL 354
 DB 347 GLQMGVESMSISSPEYPODENBSVAKQLEASVHAFGLAEIKRQKRPQKQNEAYVR 406
 QY 355 EEPSPSVKPKCSLTKRSRADEEYVQPMATG-----TSSDMAOPPOPTPST--FRNQ 407
 DB 407 EERKRRVSHDPEAQRAR---ENIKSAGARGHSDPSTSGIALVQOLSWPATOTVWNG 463
 QY 408 MESPSTGTGPPGPRKNGCAERKNNMSCRPPEPN-----PYTGRLPVN-----IY 453
 DB 464 LYNQHGFGTGTGVVYPRNLGQNTSTYTPVPEINIGSGTFPIPYSGVADDLITTF 523
 QY 454 NCSGVQVGNNTLYMQOTTLALPTKGLASGGRQLQHPVYSGQEGKPKDEANSPQCHY 513
 DB 524 NSSGIDIGHNTMDV-----GLNSQPPNNTCK---EESTSRQALTF 561
 QY 514 NNS 516
 DB 562 DWT 564

RESULT 2
 ID RIP_HUMAN STANDARD: PRT: 671 AA.
 AC 013546: 013180:
 DT 01-NOV-1997 (rel. 35, Created)
 DT 30-MAY-2000 (rel. 39, Last sequence update)
 DT 16-OCT-2001 (rel. 40, Last annotation update)
 DE Serine/threonine protein kinase RIP (BC 2.7.1.-) (Cell death protein
 RIP) (Receptor interacting protein).
 GN RIP1 OR RIP.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 NC NCB1:taid-9606;
 RN NCB1:11)
 RP SEQUENCE FROM N.A.
 RC TISSUE=umbilical vein endothelial cells;
 RX MEGPINT-96200892; PubMed-8612133;

RA Hsu H., Huang J., Shu H.-B., Balchwal V.R., Goeddel D.V.:
 RT "TNF-dependent recruitment of the protein kinase RIP to the TNF
 RT receptor-1 signaling complex."
 RT Immunity 4:387-396(1996).
 RL (2)
 RN REVISION TO 120.
 RP
 RA Hsu H., Huang J., Balchwal V.R., Goeddel D.V.:
 RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE OF 300-671 FROM N.A.
 RX MEDLINE-95277838; PubMed-7538908;
 RA Stenger B.Z., Leder P., Lee T.-H., Kim E., Seed B.:
 RT "Rip: a novel protein containing a death domain that interacts with
 RT Fas/Abd-1 (CD95) in yeast and causes cell death."
 RL Cell 81:513-523(1995).
 CC -1- FUNCTION: INTERACTS WITH THE DEATH DOMAIN OF FAS AND TRADD AND
 CC INITIATES APOPTOSIS. IT IS RECRUITED BY TRADD TO TNFRI IN A TNF-
 CC DEPENDENT PROCESS. REQUIRED FOR TNFRI ACTIVATION OF NF-KAPPA B.
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC -1- SIMILARITY: CONTAINS 1 DEATH DOMAIN.
 CC
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 CC
 CC EMBL: U50062; AAC32232.1;
 DR EMBL: U25994; AAC50137.1;
 DR HSSP: P1362; JAGW.
 DR MIM: 601453;
 DR InterPro: IPR000488; Death.
 DR InterPro: IPR000719; Euk-kinase.
 DR InterPro: IPR004040; Ser-kinase.
 DR InterPro: IPR002290; Ser-thr-kinase.
 DR InterPro: IPR001245; Tyr-kinase.
 DR Pfam: PF00531; death. 1.
 DR Pfam: PF00069; kinase. 1.
 DR PRINTS: PRO0109; TYRKINASE.
 DR SMART: SM00005; DEATH. 1.
 DR SMART: SM00221; STYK. 1.
 DR PROSITE: PS00108; PROTEIN_KINASE_ST. 1.
 DR PROSITE: PS50011; PROTEIN_KINASE_DOM. 1.
 DR PROSITE: PS50017; DEATH_DOMAIN. 1.
 DR Transferrase: Serine/threonine-protein kinase; ATP-binding;
 KM
 KW Apoptosis.
 FT NP_BIND 17 289 PROTEIN KINASE.
 FT NP_BIND 23 31 ATP (BY SIMILARITY).
 FT BINDING 49 49 ATP (BY SIMILARITY).
 FT ACT_SITE 138 138 BY SIMILARITY.
 FT DOMAIN 583 669 DEATH.
 FT DOMAIN 411 414 POLY-ARG.
 FT CONFLICT 514 514 T->S (TM REF. 3).
 SQ SEQUENCE 671 AA: 75958 MW: BA0C4E7E70456ABE CRC64:

Query Match 15.2%; Score 423; DB 1; Length 671;
 Best Local Similarity 25.3%; Pred. No. 6.5e-19;
 Matches 145; Conservative 95; Mismatches 186; Indels 146; Gaps 22;

QY 17 SIELENGEVLGKDGSTVFRAGHRKMG-----YDVAIVYNSFAISREYKMAASIDN 69
 DB 14 SSDLESAEL-DSGGGRKVSICFHRSHGVYIAKKTGTGNGRAETINEVLEEGKMMRL 72
 QY 70 EYVRLSEGVIEKVMQDQKRALVYKFMENGLSGLLQSCPPRPMLLCRLKEVYLAAC 129
 DB 73 SRVYKLGVI-----IEEGKSLVMEYKMGKLNHVKLTQIDVPLSKRHIIVEAE 127
 QY 130 YLDQNPVLLHRLDKPSNVLPPPELVKRLADFGSLTFQSGSO-----SGTSGS 177
 DB 128 YLHDKG--VIHDKLRKENTLVDRDFHRIKADLVASRTSKLTKKMDKOKEVST 184

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OY 178 EPGGILGTLAPLPELVNVRKASTADSVTSFGLMAVLAGREVELPTEPSLYEAVCMRQ 237
DB 185 NGSTGLYVNAPEHLNDVNAKPTREKSDVSPFVLMALFAKRE---EYE-----MAICEQQ 236
OY 238 -----NRPSTLAPLQAGPPTPCLEIKELMOLCWSSEPKRSPFOCLPPTDEVRO- 288
DB 237 LINCISGNRPDVIDTEICPRB-----IISMLICBAPDEARPTF-----FOIEKRRP 287
OY 289 -----AVENKNAVSTVQDFLSQLSSNRR-----SIPES----- 320
DB 288 FYLSQLEESVEEDVSKLREYSENAVVRKQSLDLCVAVPSSRSNATEPGSLHSSQ 347
OY 321 --GCGGTENDGFRRTIENOSHNDVSEMT-----NKLNLPEPSSVPRKC 365
DB 348 GLGMPVEESMFAPSLFHPQENEPISLQSLQDEANHLGSRNDQGTQGPQNVAVNR 407
OY 366 PSLLKRSRAQEEVQPA-----WTAGTSSDSMAQPR---PQPESTFRN 406
DB 408 EE-ERRRSHDPAPQAPRYENPQTECKGTVYSSASHGNAVHOPGLTSQFQVLYONN 466
OY 407 QMPG-----PTSTGT-----PS-----PGRPGNAGAEKGMNMSCHTPEP 441
DB 467 GLVSHSGFRPLDPGTAPRVYRPIPSHPSLHNFPEETVYLGNTPIEPSLPPFD 526
OY 442 NPVTGRPLVNYNCGVGVGDNNYLTMOQTA 473
DB 527 ESIR-----YTIYNSITGIGATVNYMIGTSS 554

RESULT 3
ANR3_HUMAN STANDARD: PRT; 832 AA.
AC P57078;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Serine/threonine-protein kinase ANKRD3 (EC 2.7.1.-) (Ankyrin repeat
  domain protein 3) (PKC-delta-interacting protein kinase).
GN ANKRD3 OR DK.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID:9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-20289799; PubMed-10830953;
RA Hattori M., Fujiyama A., Taylor T.D., Watanabe H., Yada T.,
RA Park H.-S., Toyoda A., Ishii K., Totsuki Y., Choi D.-K., Soeda E.,
RA Onuki M., Takegi T., Sakaki Y., Taudien S., Blechschmidt K., Polley A.,
RA Menzel U., Delabar J., Rumpf K., Lehmann R., Patterson D.,
RA Reichwald A., Rump A., Schillabel M., Schudy A., Zimmermann W.,
RA Rosenthal A., Kudoh J., Shibuya K., Kawasaki K., Asakawa S.,
RA Shintani A., Sasaki T., Nagamine K., Mitsuyama S., Antonarakis S.E.,
RA Minohima S., Shimizu N., Nordstiek G., Hornischer K., Brandt P.,
RA Schaefer M., Schoen O., Desario A., Reichelt J., Kauer G., Bloecher H.,
RA Remer J., Beck A., Klages S., Hennig S., Rieseemann L., Dagand E.,
RA Weinmeyer S., Borzym K., Gardiner K., Nizetic D., Francis F.,
RA Leberich H., Reinhardt K., Yaejo H.-L.,
RT The DNA sequence of human chromosome 21.
RL Nucleu 405311-319(2000).
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC -!- SIMILARITY: CONTAINS 10 ANK REPEATS.
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DR EMBL: AF001743; BAA95526.1; -

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DR MIM: 603706; -
DR InterPro: IPR002110; ANK.
DR InterPro: IPR000719; Euk_kinase.
DR InterPro: IPR004040; Sty_kinase.
DR InterPro: IPR002290; Ser_thr_kinase.
DR InterPro: IPR001245; Tyr_kinase.
DR Pfam: PF00023; ank; 10.
DR Pfam: PF00069; kinase; 1.
DR PRINTS: PR00109; TYRKINASE.
DR SMART: SM00248; ANK; 10.
DR SMART: SM00221; STYK; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS50297; ANK_REPEAT_REGION; 1.
DR PROSITE: PS50088; ANK_REPEAT; 9.
KW transferase; serine/threonine-protein kinase; ATP-binding; Repeat;
KW ANK repeat.
FT DOMAIN 22 286 PROTEIN_KINASE.
FT REPEAT 485 514 ANK 1.
FT REPEAT 518 547 ANK 2.
FT REPEAT 551 580 ANK 3.
FT REPEAT 584 613 ANK 4.
FT REPEAT 617 647 ANK 5.
FT REPEAT 651 680 ANK 6.
FT REPEAT 684 713 ANK 7.
FT REPEAT 717 746 ANK 8.
FT REPEAT 750 780 ANK 9.
FT REPEAT 782 811 ANK 10.
FT NP_BIND 28 36 ATP (BY SIMILARITY).
FT BINDING 51 51 ATP (BY SIMILARITY).
FT ACT_SITE 143 143 BY SIMILARITY.
SQ SEQUENCE 832 AA; 91610 MW; 508FFED5F04F7EBCB CRC64;

Query Match 14.5%; Score 401; DB 1; Length 832;
Best Local Similarity 28.4%; Pred. No. 1.9e-17;
Matches 126; Conservative 71; Mismatches 173; Indels 74; Gaps 14;

OY 10 GAPALVSTP-----ELENOELVKGDRGTGTFRAQRRMGTDVAVKYNKAIS----- 58
DB 6 GTPALALVLTFTAGERTGEMVEGSGEQVYKVRHVKTKMLAIKSPSLHVDREHNE 65
OY 59 --REVKNMASLNDNEFVLREGVIEKVNMDQDKPALVTKFENGSLGSLQSCPPMPPL 116
DB 66 LLEAKKMEAKRRTIIPYGTGR-----PVGIVNVEKMGSTLEKLASR-PLPNDL 117
OY 117 LCRLLKEVYLGMEYTLNDQNPVLIARDLPARNVLPDPPLAVKTLADFGISTFGSGSGTGS 176
DB 118 RFRITHTAVGNMFLCNAPPLHLDLKNANLIDAHYHNTISDFGLAKNGLSHSDLS 177
OY 177 GEP-GGTGLYLAPELVNVRKASTADSVTSFGLMAVLAGREVELPTEPSLYEAV-C 234
DB 178 MDGLFGITAVLTPERRIREKSRLEDFTRKHQDYSPAIYIMCVLTQK-PRADKNIHLINAV 236
OY 235 NRPSTLAPLQAGPPTPCLEIKELMOLCWSSEPKRSPFOCLPPTDEVQVNMNN 294
DB 237 VKGRPELPYCAKRR--ACSHLRLMQRCKQSDPRVRPTFQ-----GNGL 281
OY 295 NAAVSTVKDFLSQLKSSNRRFSIPESGCGGTENDGFR-----RRT 334
DB 282 NGEL--TRQVLAAL-----LPVIGRWRSFGEGFRLESEVYIIRVTCPLSPQETTSRT 331
OY 335 ENQSRNDVAVSEMTLKNLLEPPSSVPRKCSPLTKRSRA-----OEBOVQAWTACTGSSD 390
DB 332 EDLEKRDDEYKTFADLDVYKSPERSEVPARLKRAASAPTFNDVYSLELLSQDSCV 391
OY 391 SMA-OPQPTETSTFANOWSPRTS 413
DB 392 SQAVGEPBELSRSSSESKLPSGSS 415

RESULT 4

```

M3K7_HUMAN STANDARD: PRT: 606 AA.
 AC 043318; 043317; 043319;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DE MitoGen-activated protein kinase kinase 7 (EC 2.7.1.-)
 DE (transforming growth factor-beta-activated kinase 1) (TGF-beta-activated kinase 1).
 GN MAPK7 OR TAK1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
 RC TISSUE=Lung;
 RA MEDLINE=98153801; PubMed=9480845;
 RA Sakurai H., Shigemori N., Hasegawa K., Sugita T.;
 RT "TGF-beta-activated kinase 1 stimulates NF-kappa B activation by an NF-kappa B-inducing kinase-independent mechanism.";
 RL Biochem. Biophys. Res. Commun. 243:545-549(1998).
 CC -1- FUNCTION: CAN PHOSPHORYLATE AND ACTIVATE YET UNDEFINED MAPKs. MEDIATOR OF TGF-BETA SIGNAL TRANSDUCTION. STIMULATES NF-KAPPA B ACTIVATION.
 CC -1- ALTERNATIVE PRODUCTS: 3 ISOFORMS; 1A, 1B (SHOWN HERE) AND 1C; ARE PRODUCED BY ALTERNATIVE SPLICING.
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES. MAP KINASE KINASE SUBFAMILY.
 CC -1- SIMILARITY: IN THE C-TERMINAL SECTION: STRONG, TO C21OR7.
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 CC
 DR EMBL; AB009357; BAA25026.1; -
 DR EMBL; AB009356; BAA25025.1; -
 DR EMBL; AB009358; BAA25027.2; -
 DR HSSP; P00523; 2PTK.
 DR MIM; 602614; -
 DR InterPro: IPR000719; Euk_Pkinase.
 DR InterPro: IPR004040; Ser_Pkinase.
 DR InterPro: IPR002290; Ser_Thr_Pkinase.
 DR Pfam; PF00065; Pkinase; 1.
 DR SMART; SM00221; STYK; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
 DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
 KM Transferase: Serine/threonine-protein kinase; ATP-binding;
 KW Alternative splicing.
 FT DOMAIN 8 14 POLY-SER.
 FT NP_BIND 36 291 ATP (BY SIMILARITY).
 FT BINDING 42 50 ATP (BY SIMILARITY).
 FT ACT_SITE 63 63 ATP (BY SIMILARITY).
 FT ACT_SITE 156 156 BY SIMILARITY.
 FT VARSPPLIC 404 430 MISSING (IN ISOFORM 1A).
 FT VARSPPLIC 509 518 PLACPSNKE -> ISOCERTGCG (IN ISOFORM 1C).
 FT VARSPPLIC 519 606 MISSING (IN ISOFORM 1C).
 SQ SEQUENCE 606 AA; 67196 MW; 308F6147CD174013 CRC64;

Query Match 11.6%; Score 321; DB 1; Length 606;
 Best Local Similarity 26.6%; Pred. NO. 1,3e-12;
 Matches 134; Conservative 77; Mismatches 182; Indels 110; Gaps 26;

OY 11 AAPAPVLSIE-----ELENGELVGNKDGCTVFRRAQRRM-GYDAVAVKIVS---KAISRE 60
 DB 21 AFSQVINFEEIDYKEIEVEVVGRAFGVCA--KWRKDAVAKIOIESERKAFIVE 77

OY 61 VKAMASLDNEFVRLRGCV-TEKYNNDQDPRALYTKRMENSSLSGLASQDCRP----- 113
 DB 78 LKQJLSRVNHPVRLVIGACINRP-----CLVMEIAREGSLNVLKRAEPLPYTTAAH 129
 OY 114 ---WPLICRLKREVLVGMFYLLHDQNP-VLHRRDLKPSN-VLPPELVKRLADFG-----LS 164
 DB 130 AMSMVLQCS-----GQVAVLHSMQPKALIHRLDKPRLNLLVAGTVLIDCFGRACDIO 183
 OY 165 TFGQSGOSGSCGPGCTGTYLAPELFVNVRKASTASDVYSFGIILANVLAGREV--EL 222
 DB 184 THMTNNK-----GSAAMNAPEVEGSSN--YSEKCDVFSNCIILNEIVYIRRRAPPEI 232
 OY 223 PTERSLYEVANCRNRPFLAEPLQAGPETGELGKLELQVCSSEPPDRSPDECL-- 280
 DB 233 GGPAPRIMAVHNGTRPPLKRLPR-----ISLWTRKMSDPORSPRSMELIVKI 283
 OY 281 -----PKTDEVFQVY-----ENNNAAVSTYKDFLSLQKSSNRFSIPSSGCGTEM 327
 DB 284 MTLKRRFPQGADEPLQPCQYSDGQSNSATST--GSPMDIATSN-----TSNKSDTNM 335
 OY 328 DQFRT-----TENQHSNDVNVSEMLKNTLEPPSSVPKICP--SLTKRSRAQEGV 379
 DB 336 EGVPRINDTIRLESKLKQAKQSSGRLSLGASRGSYSGLPPTSGKMSADNSET 395
 OY 380 PQAWTACTSSDSMAQPPQPTSTFRN--QMPSTSTGTPSPGPRKNGAERQGNMWSGR 437
 DB 396 -EARIATVATYSRPRKGRHR-KTASFGMILDYBEIVISGNGQPRRRSIDLTYTG----- 447
 OY 438 TPEPPTVYGR---PLVNIYCSG 457
 DB 448 -TEPGOVSSSSSPSVRMITTS 469

RESULT 5
 M3K7_MOUSE STANDARD: PRT: 579 AA.
 AC 062073;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DE MitoGen-activated protein kinase kinase 7 (EC 2.7.1.-)
 DE (transforming growth factor-beta-activated kinase 1) (TGF-beta-activated kinase 1).
 GN MAPK7 OR TAK1.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=96123277; PubMed=8533096;
 RA Yamaguchi K., Shirakabe K., Shibuya H., Irie K., Ohnishi I., Ueno N., Taniguchi T., Nishida E., Matsumoto K.;
 RT "Identification of a member of the MAPKK family as a potential mediator of TGF-beta signal transduction.";
 RL Science 270:2008-2011(1995).
 CC -1- FUNCTION: CAN PHOSPHORYLATE AND ACTIVATE YET UNDEFINED MAPKs. MEDIATOR OF TGF-BETA SIGNAL TRANSDUCTION. STIMULATES NF-KAPPA B ACTIVATION.
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES. MAP KINASE KINASE SUBFAMILY.
 CC -1- SIMILARITY: IN THE C-TERMINAL SECTION: STRONG, TO C21OR7.
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 CC
 DR EMBL; D76446; BAA11184.1; -
 DR HSSP; P12931; IFMK.

DR MCD; MGI:1346877; Map3k7.
 DR Interpro: IPR000719; Euk_pkinase.
 DR Interpro: IPR004040; STY_pkinase.
 DR Interpro: IPR002290; ser_thr_pkinase.
 DR Pfam: PF00069; pkinase; 1.
 DR SMART: SM00221; STYK; 1.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
 DR PROSITE: PS0011; PROTEIN_KINASE_DOM; 1.
 DR Transferase: Serine/threonine-protein kinase; ATP-binding.
 KW DOMAIN 8 16 POLY-SER.
 FT DOMAIN 36 291 PROTEIN KINASE.
 FT NP_BIND 42 50 ATP (BY SIMILARITY).
 FT BINDING 63 63 ATP (BY SIMILARITY).
 FT ACT_SITE 156 156 BY SIMILARITY.
 SO SEQUENCE 579 AA; 64227 MW; 97CB6F3CB8283EE CRC64;

Query Match 11.3%; Score 312.5; DB 1; Length 579;
 Best Local Similarity 25.4%; Pred. No. 3,4e-12;
 Matches 126; Conservative 77; Mismatches 170; Indels 123; Gaps 24;

QY 11 APALVSI-----ELENDLVKDGCTVRAORRW-GYDAVKIVNS---KAISRE 60
 DB 21 APSQVLFEEIDYKKEIEVEYVGRCAFGVCKA---KRAKDVAIKIQISESBRKATVE 77
 QY 61 VKMAASLDNFTVLRGV-IEVNMDOOPRALYTKRMENGSLSGLSQCRRP----- 113
 DB 78 LROSLRNHNRYKLGACLNRY-----CLVMTABSGSLNVHGAEPYPTTAAN 129
 QY 114 ---WPLLCRLKLVGLMEYLDONP-VLHARDKPSN-VLPPELRYVLADFG-----LS 164
 DB 130 AMSQCLOGS-----OCVAYLHSDPKALHRRDKPRLNLLVAGVYLKICDFGTCDIQ 183
 QY 165 TPQGSQSGSGSGEPGTGLYAPLPELVNVRKASTADYVSFGIIMVAVIAGREY--EL 222
 DB 184 THRTNKK-----GSAAMNAPVEFGSN--YSEKCDVFSNGITIMEYIIRKRPDEI 232
 QY 223 PTEPSLYEAVCNCRNRPSELAPLPOAGETGCLGELKELMQLWSSBPDRSPQCL-- 280
 DB 233 GGPAPRLMNVHNGRPPPLIKRLPP-----ISLWTRQMSDPQORPSMEIYKI 283
 QY 281 -----PKTDEVFQNV-----ENNNNAVSTVKDELSQLKSNRFRSPESGOGTE 327
 DB 284 MTHLMRYFPADDEPLQYPCOYSDGOSNATST-----GSPM 320
 QY 328 DGFRRRTIENOHSDNVNVEMLNKLSEPPSS--VPRKCPSLTKRSRAOEGVQAWTA 385
 DB 321 D-----IASNTSK-----SDPMQGVATNDITKRLSKLKNQAKQSSBSGRSL 368
 QY 386 GTSSDSMAOPQOTPETSTFRNHPSPSTGTGPPGPRGN--GGAERQGMNMSCRTPPNPV 444
 DB 369 GAARGSSVE--SLPPTSEGRMSADMSIEARIYATAGNGOPRRRSIODLVGTGTEPGOV 426
 QY 445 TGR---PLVNIYVNCSC 457
 DB 427 SSRSSPSVKNITGSC 442

RESULT 6
 M3KA_HUMAN STANDARD: PRT; 954 AA.
 AC 002779; 012761; Q14871;
 DT 01-FEB-1994 (Rel. 28; Created)
 DT 30-MAY-2000 (Rel. 39; Last sequence update)
 DT 16-OCT-2001 (Rel. 40; Last annotation update)
 DE Mitogen-activated protein kinase kinase kinase 10 (EC 2.7.1.37)
 DE (Mixed lineage kinase 2) (Protein kinase MST).
 GN MAP3K10 OR M1K2 OR MST.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 NX NCBI_TaxId=9606;

RM [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-Brain;
 RX MEDLINE-96128179; PubMed-8536694;
 RA Dorew D.S., Devereux L., Tu G.F., Price G., Nicholl J.R.,
 RA Sutherland G.R., Simpson R.J.;
 RT "Complete nucleotide sequence; expression, and chromosomal
 RT localisation of human mixed-lineage kinase 2.";
 RL Eur. J. Biochem. 234:492-500(1995).
 RM [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE-Brain;
 RX MEDLINE-95249256; PubMed-7731697;
 RA Katoch M., Hirai M., Sugimura T., Terada M.;
 RT "Cloning and characterization of MST, a novel (putative)
 RT serine/threonine kinase with SH3 domain.";
 RL Oncogene 10:1447-1451(1995).
 RM [3]
 RP SEQUENCE OF 244-480 FROM N.A.
 RC TISSUE-Colon epithelium;
 RX MEDLINE-9328756; PubMed-8477742;
 RA Dorew D.S., Devereux L., Dietzsch E., de Kretser T.;
 RT "Identification of a new family of human epithelial protein kinases
 RT containing two leucine/isoleucine-zipper domains.";
 RL Eur. J. Biochem. 213:701-710(1993).
 CC -1- CATALYTIC ACTIVITY: ATP + a protein -> ADP + a phosphoprotein.
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN BRAIN AND SKELETAL MUSCLE.
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC -1- MAP KINASE KINASE SUBFAMILY.
 CC -1- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
 CC -----
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 CC or send an email to license@sib-sib.ch).
 CC -----
 DR EMBL; X90846; CAAC2351.1; -;
 DR EMBL; X44615; CAAC8531.1; -;
 DR PIR; S32468; S32468.
 DR HSSP; P29355; ISEM.
 DR MIM; 600137; -;
 DR Interpro: IPR000719; Euk_pkinase.
 DR Interpro: IPR001452; SH3.
 DR Interpro: IPR004040; STY_pkinase.
 DR Interpro: IPR002290; Ser_thr_pkinase.
 DR Interpro: IPR001245; Tyr_pkinase.
 DR Pfam; PF00069; pkinase; 1.
 DR PRINTS; PR00452; SH3DOMAIN.
 DR PRINTS; PR00109; TYRKINASE.
 DR SMART; SM00326; SH3; 1.
 DR SMART; SM00221; STYK; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
 DR PROSITE; PS0011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00002; SH3; 1.
 KW Transferase: Serine/threonine-protein kinase; Tyrosine-protein kinase;
 KW ATP-binding; SH3 domain.
 FT DOMAIN 2 5
 FT DOMAIN 16 81
 FT NP_BIND 98 360
 FT NP_BIND 104 112
 FT BINDING 125 125
 FT ACT_SITE 222 222
 FT DOMAIN 384 405
 FT DOMAIN 419 440
 FT DOMAIN 449 463
 FT CONFLICT 462 464
 FT CONFLICT 465 480
 FT
 POLY-GLU.
 SH3.
 PROTEIN KINASE.
 ATP (BY SIMILARITY).
 ATP (BY SIMILARITY).
 BY SIMILARITY.
 LEUCINE-ZIPPER (BY SIMILARITY).
 LEUCINE-ZIPPER (BY SIMILARITY).
 ARG/LYS-RICH (BASIC).
 SER -> AV (IN REF. 2).
 LKLEGGSHISLPSGF -> AQAAGRPPPALMTL (IN
 REF. 3).

FT CONFLICT 471 471 G -> S (IN REF. 2).
 FT CONFLICT 807 807 G -> R (IN REF. 2).
 FT CONFLICT 818 818 V -> A (IN REF. 2).
 SO SEQUENCE 954 AA: 103623 MW: 53864AAAS59B0ABA CRC64;

Query Match 10.9%, Score 303; DB 1; Length 954;
 Best local similarity 22.8%, Pred. No. 2,4e-11;
 Matches 150; Conservative 85; Mismatches 223; Indels 200; Gaps 32;

OY 4 VILVMS-----GAPALVSI-----ELENOELVKGKCECTVRAOHRKRGDVAVK 50
 DB 68 VGVFSSNYVAPCAPAPAPAGLDPOEIPHEIQLLEIIIVGVGKFRVRLALMR--GEQVAK 125
 OY 51 -----IYNSKAIKREYKAAASLDNEFVLECEVKEVNMDDPPKALVTFEMENG 100
 DB 126 AARLDPEKPAATADVOCDEARLFCALQHPHIIILRACU-----NPHILCLVMEYARCG 180
 OY 101 SLGGLQSCPPRPPLCLRLKEVYLGHFYLDQNPV--LRLDLKPSN--VLDPPELH-- 155
 DB 181 ALSRLVLAGRRVP--HYLVNMAVNOVARGNMTHNDAPPIIIRDLKSNILILILEATENHL 239
 OY 156 ----VTLADFGSLTSGOSOSTSGSGRGCTGLTALAE-----LFVNRKASTADVYS 206
 DB 240 ADTVLKLITDFGLAR-----EMKRTKMSAGTYANMADEVIRLSLF-----SKSDVMS 288
 OY 207 FCIIMAVVLAG---REVELPTEPSLYEAVCNQNPRLSLAEIPQAGPETPGLGLEKELM 262
 DB 289 FGVLLMELLTGEVPREID---ALAVAGVAMRLTLP---IPSTCPSP-----FARLL 336
 OY 263 QLCNSEPPDRSPFOECIPKTD-----EYQVQENNNMAVSTVDFL-----S 306
 DB 337 EECNPDPRGRDRFGSILKRLKLEVIQSLAFQMPRESHSIQZMKLEFIQMDOLRTKCR 396
 OY 307 QLKSSNRNFSIPESQGGTEMDGERRTIENDSHNDVASE---WLNKLINLEP----- 357
 DB 397 ELRSREELRLAAQDQROBEQRLRRREBELAREMDIVLEELMLKQCSQSKPRVRRKR 456
 OY 358 -----PSVYPRK-----CPLTKRSRAQEDVPOAMTAGTSSDM 392
 DB 457 GNFRRSLKLKREGSHISLPSGFHRTITVQASPTLKKR-----GSGG- 500
 OY 393 AOPPOPE--TSTFRNQNSPTSTGTPSPG-----PRGNO--GAEQGMMS 435
 DB 501 ASPPASPSTIPLRLAIRLTPVDCGSSSGSSGSGSGTWSRGPKEELVGKRGKRTWG 560
 OY 436 -CRTEBPNPVTCGRPLVNTYNCQVOVDNNYLTNQOTLALPTGLAP----- 481
 DB 561 PESTLQKEVGGEE-----RLKGLDEG-----SKOMSSAPNLGKSPKHTPIAPGASLN 610
 OY 482 -----SGNGRGLQHP-----PVGSQSGCPMDPEAM-----SROGMVNHSGK 518
 DB 611 EMEERAEADGGSSVPPSPSTPSYLSVPLAPRSPCARAPAPWPTPSAPRANHGCR 668

RESULT 7
 CTRL_ARATH STANDARD; PRT; 821 AA.
 AC 005609;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Serine/threonine-protein kinase CTRL (EC 2.7.1.37).
 GN CTRL OR AT5G03730 OR F17C15_150.
 OS Arabidopsis thaliana (mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsie.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. COLUMBIA; TISSUE=Seedling;
 RX MEJLINE-93161417; Pubmed-8431946;

RA Kieber J.J., Rothenberg M., Roman G., Feldmann K.A., Ecker J.R.;
 RT "CTRL", a negative regulator of the ethylene response pathway in
 RT Arabidopsis, encodes a member of the Raf family of protein kinases.
 RT Cell 72:427-441(1993).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. COLUMBIA;
 RX MEJLINE-21016721; Pubmed-11130714;
 RA Tabata S., Kaneko T., Nakamura Y., Kotani H., Kato T., Asanizu E.,
 RA Miyajima N., Sasamoto S., Kimura T., Hosouchi T., Kawashima K.,
 RA Kohara M., Matsumoto M., Matsuno A., Murai A., Nakayama S.,
 RA Nakazaki N., Naito K., Okamura S., Shino S., Takeuchi C., Wada T.,
 RA Narazaki N., Tameda K., Yasuda M., Sato S., de la Bastide M.,
 RA Huang E., Spiegel L., Gnoj L., O'Shaughnessy A., Preston R.,
 RA Haberman K., Murray J., Johnson D., Rohlfing T., Nelson J.,
 RA Stoneking T., Pepin K., Spieth J., Sekhon M., Armstrong J., Becker M.,
 RA Belter E., Cordum H., Cordes M., Courtney B., Courtney W., Datta M.,
 RA Du H., Edwards J., Fryman J., Haakensen B., Lamar E., Latrelle P.,
 RA Leonard S., Meyer R., Mulvaney E., Ozersky P., Riley A., Stromatt C.,
 RA Wagner-McPherson C., Wollam A., Yeakum M., Bell M., Dedha N.,
 RA Patneil L., Shah R., Rodriguez M., Hoon See L., Vill D., Baker J.,
 RA Kirchoff K., Roth K., King L., Bahret A., Miller B., Marra M.,
 RA Martienssen R., McCombie W.R., Wilson R.K., Murphy G., Bancroft I.,
 RA Vokacert G., Mambo R., Duesterhoef A., Stiekema W., Pohl T.,
 RA Enlhan K.-D., Terryn N., Hartley N., Bent E., Johnson S.,
 RA Langham S.-A., McCullagh B., Robben J., Grymoprez B., Zimmermann W.,
 RA Ramberger U., Medler H., Balke K., Medler E., Peters S.,
 RA van Staveren M., Dirse W., Noeljan P., Klein Lankhorst R.,
 RA Weltzenegger T., Botke G., Rose M., Hauf J., Bernerleiser S., Hempel S.,
 RA Feldpausch M., Lamberth S., Valleroel R., Gelen J., Ardiles W.,
 RA Berts O., Lemcke K., Kolesov G., Meyer K.F.X., Rued S., Schoof H.,
 RA Schueller C., Zaccaria P., Meves H.-W., Bevon M., Franz P.F.;
 RT "Sequence and analysis of chromosome 5 of the plant Arabidopsis
 RT thaliana."
 RT Nature 408:823-826(2000).
 RT Nature 408:823-826(2000).
 CC -1- FUNCTION: ACTS AS A NEGATIVE REGULATOR IN THE ETHYLENE RESPONSE
 CC PATHWAY.
 CC -1- CATALYTIC ACTIVITY: ATP + a protein - ADP + a phosphoprotein.
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN BOTH SEEDLINGS AND ADULT PLANTS.
 CC -1- MISCELLANEOUS: CTRL MUTANTS DISPLAY ETHYLENE-TREATED PHENOTYPES,
 CC RESULTING IN PLANTS WITH SMALL, UNEXPANDED LEAVES AND SHORT SEED
 CC COTYLEDON GROWTH IS IMPAIRED.
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC MTL/RAF SUBFAMILY.
 CC -----
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 CC -----
 CC EMBL: L08789; AAA32779.1;
 CC EMBL: L08790; AAA32780.1;
 CC EMBL: A1162506; CAB82938.1;
 CC HSSP: A11362; 1EGR.
 CC InterPro: IPR000719; Euk_Pkinase.
 CC InterPro: IPR004040; STY_Pkinase.
 CC InterPro: IPR002290; Ser_thr_Pkinase.
 CC Pfam: PF00069; pkinase.1.
 CC SMART: SM00221; STYCK.1.
 CC PROSITE: PS00107; PROTEIN_KINASE_ATP.1.
 CC PROSITE: PS00108; PROTEIN_KINASE_ST.1.
 CC PROSITE: PS50011; PROTEIN_KINASE_DOM.1.
 CC Transferrase: Serine/threonine-protein kinase; ATP-binding.
 CC DOMAIN 65 69 POLY-GLY.
 CC DOMAIN 135 141 POLY-GLY.
 CC DOMAIN 551 809 PROTEIN KINASE.
 CC NP_BIND 557 565 ATP (BY SIMILARITY).
 CC BINDING 578 578 ATP (BY SIMILARITY).
 CC ACT_SITE 676 676 BY SIMILARITY.
 CC MOTAGEN 596 596 E->K: IN CTRL 4; EXHIBITS ETHYLENE-

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FT      TREATED PHENOTYPE.
FT      MOTAGEN      694      694      D->: IN CTRL-1; EXHIBITS ETHYLENE-
FT      SEQUENCE      821 AA: 90306 MW; .292203DCDDCC1SBC CRC64; TREATED PHENOTYPE.
SQ

Query Match      10 98; Score 302; DB 1; Length 821;
Best Local Similarity 33.68; Pred. No. 2.3e-11;
Matches 92; Conservative 44; Mismatches 96; Indels 42; Gaps 12;

OY      20 ELENQELVGEKDGFTVFAQHRKQ-GYDAVKIYNSK-----AISREVMASLDNE 70
DB      550 DLIKKIKIGSGFTGVHRAE---WEGSDVAVKILMEQDFHAEVNEFLREVMIRLHNP 606
OY      71 FVRLGVEIEKVMDDPFPALVTKFMENGLSGLOSQCPRRWPLLCRLK---EVLG 127
DB      607 NIYLPFGAV-----QPPMLSTVTEYLSRGLYRLHLSKARQDLDBRRRLSMAYDAVK 661
OY      128 MFTLHQNPVLLHRLDKPSNVLPPDELHVKLADFGLSFGGSGSGSGSGGEGTLYLA 187
DB      662 MNYLHNRNPPIVHRLDKSPNLLVDKRYVVCDFGLSLRK--ASTLSKSAAGTPEWMA 719
OY      188 PELFVNNKASTASDVYSFGILMAVLAGREVELPEPELVYEA---CNQNPISLAE 244
DB      720 PE--VLRDPSNKRSDVYSFGVILMELATLQPGMGNLNPAAVVAAGFCRKR-----LE 771
OY      245 LRP-AGPEPPG-LBGLKELMDLCSSEPKORPS 276
DB      772 IPRNLNPVAAIIEG-----CMTNEPKRPSF 798

RESULT      8
TEST_RAT
ID      TEST_RAT      STANDARD:      PRT:      628 AA.
AC      063572:
DT      01-NOV-1997 (Rel. 35, Created)
DT      01-NOV-1997 (Rel. 35, Last sequence update)
DT      16-OCT-2001 (Rel. 40, Last annotation update)
DE      Testis-specific protein kinase 1 (EC 2.7.1.1-).
GN      TESTK.
OS      Rattus norvegicus (Rat).
OC      Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX      NCBI_TaxID=10116;
RN      (1)
RP      SEQUENCE FROM N.A.
RC      STRAIN=NISSAR; TISSUE=Testis;
RX      MEDLINE=96125123; PubMed=8537404.
RA      Yoshima J., Ohashi K., Okano I., Nunoue K., Kishiohara M., Kuma K.-I.,
RT      Miyata T., Hirai M., Baba T., Mizuno K.;
RT      Identification and characterization of a novel protein kinase,
RT      TESTK, specifically expressed in testicular germ cells."
RL      J. Biol. Chem. 270:31331-31337(1995).
CC      -1- FUNCTION: DISPLAYS SERINE/THREONINE-SPECIFIC PHOSPHORYLATION OF
CC      MYELIN BASIC PROTEIN (MBP) AND HISTONE IN VITRO. PROBABLY PLAYS A
CC      CENTRAL ROLE AT, AND AFTER THE MEIOTIC PHASE OF SPERMATOGENESIS.
CC      -1- TISSUE SPECIFICITY: SPECIFICALLY EXPRESSED IN TESTICULAR GERM
CC      CELLS.
CC      -1- DOMAIN: THE EXTRACATALYTIC C-TERMINAL PART IS HIGHLY RICH IN
CC      PROLINE RESIDUES.
CC      -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC      -----
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC      entities requires a license agreement (See http://www.ebi.ac.uk/announcements/
CC      or send an email to license@ebi.ac.uk).
CC      -----
DR      EMBL: D50864; BAA09460.1; .
DR      HSP: P11362; IAGP.
DR      InterPro: IPR000719; Euk_Pkinase.

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DR      InterPro: IPR004040; STY_pkinase.
DR      InterPro: IPR001245; TYR_pkinase.
DR      Pfam: PF00069; Pkinase; 1.
DR      SMART: SM00221; STYK; 1.
DR      PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR      PROSITE: PS00109; PROTEIN_KINASE_TYR; 1.
DR      PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
KM      Transferrase; Serine/threonine-protein kinase; ATP-binding.
FT      TRANSFERASE; 52
FT      NP_BIND 58 66
FT      BINDING 71 71
FT      ACT_SITE 170 170
FT      AC_SITE 170 170
SQ      SEQUENCE 628 AA: 67987 MW; F05F67FBD934B9AD CRC64;

Query Match      10 78; Score 295.5; DB 1; Length 628;
Best Local Similarity 23.38; Pred. No. 4.1e-11;
Matches 133; Conservative 82; Mismatches 213; Indels 143; Gaps 25;

OY      11 APALVSIIELENOELVGDGFTVFAQHRKQGYDAVKI---VNSKAISREVMAS 66
DB      42 AVSSILARVDPDFCAEKIGAGFSEYVKVRRHQGVVALLKMKLPSRSNSTLAEVDLMNR 101
OY      67 LDNEFVRLGVEIEKVMDDPFPALVTKFMENGLSGLOSQCPRRWPLLCRLKLEVL 126
DB      102 LRHNPRIIRFNGVCY---HGGQLHAL-TEYANGTLEGLSSPEPLSHVRLHLDLQ 156
OY      127 GMFTLHQNPVLLHRLDKPSNVL---PPELHVKLADFGLS---TFGSGSGSGSGGEP 179
DB      157 GLRRLHAKG--VEHRLDTSKNCLYRREDGFTAVAGDFGLAEKIPYREGARK-----EP 209
OY      180 GGTLSG---YLAPELFVN--VNNKASTASDVYSFGILMAVLAGREVELPEPELVYEA 234
DB      210 LAVVGSPPYHAPVFLNGELYDEKA---DVPAFGIVLCETIA---RVADPDY----- 255
OY      235 NNRKPSLAEPLAQGPPEPGLESLKE-----LMQDCHSSSEPKORPSFOBLKPTDE 285
DB      256 -----LPTDEFGLDVPAFTLVGNCPLPELILAIHCCSHESAPRAFTYITQHLQ 308
OY      286 VFOVTEENHNAAVSTYKDLISQAKSNRRFSIPESGGGEGTEMDGFRRTINQHSRDVNV 345
DB      309 ILEQLPEPTPLA---KMLPAPRLTINOGSVPRGGSAT-----LPRSDPL 352
OY      346 SEMLNKILNEPPSVKRCPSLTK-----RSR 373
DB      353 SRSRSDLELPSPSPSPSMGMDLTVNPFSLREDLRGKIKLDTDPCKPATPLVLPSP 412
OY      374 AQEQVYQAMTAGTSSDSAP-----PQPTSTFRNQMPSTGTGSPSGPRG 423
DB      413 LTSTQLPLV---ASPESLVQPEPTVPRCRSLPSPE-----LPRMETALPGFSP 461
OY      424 NQGAERQGNMNSCRTEPPNVTGRPLVNIYNCSGVYGDVNNITLMQOTYALPTMGLAPSG 483
DB      462 VGPSTEERMKCEGSSPEPPAPQPLP-----AVATDNFISTCSSASQP-WSARP-- 512
OY      484 KGRGLQHPPP---VGSQEG-PRDPAWASRP 510
DB      513 -GPSLANNPPAVYVNSPQSHARP--NNRAQ 540

RESULT      9
AVR2_SHEEP
ID      AVR2_SHEEP      STANDARD:      PRT:      513 AA.
AC      028560;
DT      01-NOV-1997 (Rel. 35, Created)
DT      01-NOV-1997 (Rel. 35, Last sequence update)
DT      16-OCT-2001 (Rel. 40, Last annotation update)
DE      Activin receptor type II precursor (EC 2.7.1.37) (ACTR-II).
GN      ACTR2 OR ACTR11.
OS      Ovis aries (Sheep).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC      Bovidae; Caprinae; Ovis.

```

NCBI_TaxID=9940;
 RN SEQUENCE FROM N.A.
 RC STRAIN=ROMNEY; TISSUE=Ovarian follicle;
 RA Tisgall D.J.;
 RL Submitted (Mar-1996) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: RECEPTOR FOR ACTIVIN A, ACTIVIN B, AND INHIBIN A.
 CC INVOLVED IN TRANSMEMBRANE SIGNALING.
 CC -1- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC TGF β RECEPTOR SUBFAMILY.
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 CC
 DR EMBL: L19442; AAA1903.1; -
 DR HSP: P27038; 18RE.
 DR InterPro: IPR000333; ActivinII_receptor.
 DR InterPro: IPR000472; Activin.rec.
 DR InterPro: IPR000719; Euk_Pkinase.
 DR InterPro: IPR002290; Ser_thr_Pkinase.
 DR Pfam: PF01064; Activin_recp.1.
 DR Pfam: PF00653; Pkinase.1.
 DR PRINTS: PR00653; ACTIVIN2R.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; FALSE_NEG.
 DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
 DR PROSITE: PS0011; PROTEIN_KINASE_DOM; 1.
 DR Receptor: Transferrase; Serine/threonine-protein kinase; ATP-binding;
 KM Transmembrane; Glycoprotein; Signal.
 FT SIGNAL 1 19
 FT CHAIN 20 513
 FT DOMAIN 136 161
 FT TRANSMEM 162 161
 FT DOMAIN 192 485
 FT NP_BIND 198 206
 FT BINDING 219 219
 FT ACT_SITE 322 322
 FT CARBOHYD 43 43
 FT CARBOHYD 66 66
 FT SEQUENCE 513 AA: 57768 MW: 731859585CA57E3 CRC64;
 Query Match 10.68; Score 294.5; DB 1; Length 513;
 Best Local Similarity 30.18; Pred. No. 3.7e-11;
 Matches 99; Conservative 56; Mismatches 125; Indels 49; Gaps 15;
 QY 12 PAPVLSIELENOELVGRDGFQVFAHNRMGVDVAVKIV-----NSKAISREYKAAAS 66
 DB 183 PSLPLGLPDLQLELVKANGSGCYVMKNO--LLENYAVKTRFPIDQDSQNMNEYEYSLRG 240
 QY 67 LNEVFVLEGVIEKVNMDOPKDALYTKRMNGSLGLSQCPRPPLRLRLKEVYL 126
 DB 241 MNEHILDTIGL-ERKGTSGVYDMLTATPRHSGSSDFKNAVY-SMNELCIHAEIEMAR 298
 QY 127 GNEVYLD-----QNEVLLRDLRKSNVLPPELHYKLADGSLG-TRFGGSGSGTSG 177
 DB 299 GLAYLHEPIGCLDKGHRPAISHRDISKSNVLLKNNLTACIADGLAKLEACKSGADRHG 358
 QY 178 EPGGTLGLYLAPELF---VNVNRKASTASDVYSFGILMNVLAGR-----EVELP-- 223
 DB 359 QY-GTKRRMAPVLEGAIRNFORDAFLAIDHYAMGLVME-LASRCIADGPDVETIMLEFV 416
 QY 224 ----TEPSL--VTEAVCKRONRPSLAELPAGPEPTGLBLKELMQLCNSSEPKRPSFQ 277
 DB 417 EEIGHPSLIEDQEVVYVHKRPRVLRDYNQ--KLGMKMLCETIEECWDHDAEKLRS-A 472

QY 278 ECLPKTDEVPOVWENNNAVSTVDFLS 306
 DB 473 GCVCERITQKQRLFN-----ITTEDIVT 496
 RESULT 10
 ID AVR2_RAT STANDARD; PRT; 513 AA.
 AC P38444;
 DT 01-OCT-1994 (Rel. 30, Created)
 DT 01-OCT-1994 (Rel. 30, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Activin receptor type II precursor (EC 2.7.1.37) (ACTR-II).
 GN ACTR2 OR ACTRII.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=SPRAGUE-DAWLEY; TISSUE=Testis;
 RX MEDLINE=93279247; PubMed=7916681;
 RA Feng Z.M., Madigan M.B., Chen C.L.C.;
 RT "Expression of type II activin receptor genes in the male and female
 RT reproductive tissues of the rat.";
 RL Endocrinology 132:2593-2600(1993).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Ovary;
 RX MEDLINE=93050162; PubMed=1385212;
 RA Shinokaki H., Ito I., Hasegawa Y., Nakamura K., Igarashi S.,
 RA Nakamura M., Miyamoto R., Eto Y., Ibuli Y., Minegishi T.;
 RT "Cloning and sequencing of a rat type II activin receptor.";
 RL FEBS Lett. 312:53-56(1992).
 CC -1- FUNCTION: RECEPTOR FOR ACTIVIN A, ACTIVIN B, AND INHIBIN A.
 CC INVOLVED IN TRANSMEMBRANE SIGNALING.
 CC -1- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC TGF β RECEPTOR SUBFAMILY.
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 CC or send an email to license@isb-sib.ch).
 CC
 DR EMBL: L10639; AAA0674.1; -
 DR EMBL: S48190; AAB23958.1; -
 DR HSP: P27038; 18RE.
 DR InterPro: IPR000333; ActivinII_receptor.
 DR InterPro: IPR000472; Activin.rec.
 DR InterPro: IPR000719; Euk_Pkinase.
 DR InterPro: IPR002290; Ser_thr_Pkinase.
 DR Pfam: PF01064; Activin_recp.1.
 DR Pfam: PF00653; Pkinase.1.
 DR PRINTS: PR00653; ACTIVIN2R.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; FALSE_NEG.
 DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
 DR PROSITE: PS0011; PROTEIN_KINASE_DOM; 1.
 DR Receptor: Transferrase; Serine/threonine-protein kinase; ATP-binding;
 KM Transmembrane; Glycoprotein; Signal.
 FT SIGNAL 1 19
 FT CHAIN 20 513
 FT DOMAIN 136 161
 FT TRANSMEM 162 161
 FT DOMAIN 192 485
 FT NP_BIND 198 206
 FT BINDING 219 219
 FT ACT_SITE 322 322
 FT BY SIMILARITY.

FT CARBOHYD 43 43 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 66 66 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CONFLICT 165 165 M -> K (IN REF. 2).
 FT CONFLICT 218 218 V -> I (IN REF. 2).
 FT CONFLICT 353 353 G -> A (IN REF. 2).
 FT CONFLICT 475 475 L -> V (IN REF. 2).
 SO SEQUENCE 513 AA: 57892 MW: C63A8742EF91DD7D CRC64;

Query Match 10.5%; Score 292.5; DB 1; Length 513;
 Best Local Similarity 29.8%; Pred. No. 4.9e-11;
 Matches 98; Conservative 55; Mismatches 127; Indels 49; Gaps 14;

QY 12 PAPVLSIELENOELVKGDFGVFAORHKGVDVAVKIV-----NSKAIISREVKAMAS 66
 DB 183 PSLPLGKPLQLLEVKARGRFCGVWKAQ--LLNEVAVAKIPIPIIDKQSMQNEVEVYSLPG 240
 QY 67 LDNEFVRLBEGVIERVKNODPKPALVYTFMENGSLGSLQSOCPRPVPLLCRLKEVYL 126
 DB 241 MKHENILOFIGA-EKRGTSVDVDMLTITAFHEKSLSDPLKANYV-SMNEICHIATETMAR 298
 QY 127 GMFYLD-----ONPVLLHRDLKPSNVLPDEPLHVKLADFGLS-TFQGSQSGTGSG 177
 DB 299 GLAYLHEDIPGLKDGHRPAISHRDIKSNVLLKNNITFCIADFLALKEPAGKSGDTHG 358
 QY 178 EPGGTGLYLAPELF--VVVNRKASTADVYSPGILMAVAVLAGR-----E 219
 DB 359 QV-STRRYMAPVYLEGAINFORDAFLRIDVYAMGLVYME-LASRCTAADGPVDEYMLPPE 416
 QY 220 VELTPESL--VYEVANCNQRPSLAELPQACPEPTGLGELKELMOUCSSEPKDRPSFO 277
 DB 417 BEIGOHSLDEMOEVVYHKKRPVLDYWG--KHAGAMLCETIECDMDHAEARLS-A 472
 QY 278 ECLPKTDEVFQVNNMNAVSTVDFLS 306
 DB 473 GCLGERITOMORLTN-----ITTEDIVT 496

RESULT 11
 AVR2_BOVIN STANDARD; PRT; 513 AA.

AC Q280A3;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Activin receptor type II precursor (EC 2.7.1.37) (ACTR-II).
 OS ACVR2 OR ACTRII.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 NC NCBI_TaxId=9113;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=HOLSTEIN; TISSUE=Testis;
 RX MEDLINE=95203477; PubMed=7534730;
 RA Ehlhar J.F., Houde A., Lussier J.G., Silverstein D.W.;
 RT "Bovine activin receptor type II cDNA: cloning and tissue
 expression.";
 RT Mol. Cell. Endocrinol. 106:1-8(1994).
 RL [2]
 RN SEQUENCE FROM N.A.
 RC TISSUE=Ovary;
 RX MEDLINE=97032546; PubMed=8675905;
 RA Montaguado L.V., Heriz A., Flavin N., Rogers M., Ennis S.,
 RA "Fluorescent in situ localization of the bovine activin receptor type
 RT IIA locus on chromosome 2 (2q3.3-2.4).";
 RL Mamm. Genome 7:869-869(1996).
 CC -1- FUNCTION: RECEPTOR FOR ACTIVIN A, ACTIVIN B, AND INHIBIN A.
 CC INVOLVED IN TRANSMEMBRANE SIGNALING.
 CC -1- CATALYTIC ACTIVITY: ATP + a protein -> ADP + a phosphoprotein.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.

-1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 TGBR RECEPTOR SUBFAMILY.

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 or send an email to license@sib-sib.ch).

DR EMBL: L21717; AAA74597.1; -
 DR EMBL: U43208; AAC48694.1; -
 DR HSSP: P27038; 18TE.
 DR InterPro: IPR000333; ActivinIL_receptor.
 DR InterPro: IPR000472; Activin_rec.
 DR InterPro: IPR000719; Euk_Pkinase.
 DR InterPro: IPR002290; Ser_Thr_Pkinase.
 DR Pfam: PF01064; Activin_recpt.1.
 DR Pfam: PF00069; Pkinase.1.
 DR PRINTS: PR00653; ACTIVINR.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP_FALSE_NEG.
 DR PROSITE: PS00108; PROTEIN_KINASE_ST.1.
 DR PROSITE: PS50011; PROTEIN_KINASE_DOM.1.
 KW Receptor; Transferase; Serine/threonine-protein kinase; ATP-binding;
 KW Transmembrane; Glycoprotein; signal.
 FT SIGNAL 1 19
 FT CHAIN 20 513
 FT DOMAIN 20 513 ACTIVIN RECEPTOR TYPE II.
 FT TRANSMEM 136 161 EXTRACELLULAR (POTENTIAL).
 FT DOMAIN 162 513 POTENTIAL.
 FT DOMAIN 192 485 CYTOPLASMIC (POTENTIAL).
 FT NP_BIND 198 206 PROTEIN KINASE.
 FT BINDING 219 219 ATP (BY SIMILARITY).
 FT ACT_SITE 322 322 ATP (BY SIMILARITY).
 FT CARBOHYD 43 43 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 66 66 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SO SEQUENCE 513 AA: 57951 MW: C2969A54CF00617B CRC64;

Query Match 10.5%; Score 290.5; DB 1; Length 513;
 Best Local Similarity 29.5%; Pred. No. 6.5e-11;
 Matches 97; Conservative 57; Mismatches 126; Indels 49; Gaps 14;

QY 12 PAPVLSIELENOELVKGDFGVFAORHKGVDVAVKIV-----NSKAIISREVKAMAS 66
 DB 183 PSLPLGKPLQLLEVKARGRFCGVWKAQ--LLNEVAVAKIPIPIIDKQSMQNEVEVYSLPG 240
 QY 67 LDNEFVRLBEGVIERVKNODPKPALVYTFMENGSLGSLQSOCPRPVPLLCRLKEVYL 126
 DB 241 MKHENILOFIGA-EKRGTSVDVDMLTITAFHEKSLSDPLKANYV-SMNEICHIATETMAR 298
 QY 127 GMFYLD-----ONPVLLHRDLKPSNVLPDEPLHVKLADFGLS-TFQGSQSGTGSG 177
 DB 299 GLAYLHEDIPGLKDGHRPAISHRDIKSNVLLKNNITFCIADFLALKEPAGKSGDTHG 358
 QY 178 EPGGTGLYLAPELF--VVVNRKASTADVYSPGILMAVAVLAGR-----E 219
 DB 359 QV-STRRYMAPVYLEGAINFORDAFLRIDVYAMGLVYME-LASRCTAADGPVDEYMLPPE 416
 QY 220 VELTPESL--VYEVANCNQRPSLAELPQACPEPTGLGELKELMOUCSSEPKDRPSFO 277
 DB 417 BEIGOHSLDEMOEVVYHKKRPVLDYWG--KHAGAMLCETIECDMDHAEARLS-A 472
 QY 278 ECLPKTDEVFQVNNMNAVSTVDFLS 306
 DB 473 GCVGERITOMORLTN-----ITTEDIVT 496

RESULT 12
 AVR2_HUMAN STANDARD; PRT; 513 AA.
 ID AVR2_HUMAN
 AC P27037; Q92474;

01-AUG-1992 (rel. 23, Created)
 01-AUG-1992 (rel. 23, Last sequence update)
 16-OCT-2001 (rel. 40, Last annotation update)
 Activin receptor type II precursor (EC 2.7.1.37) (ACTR-II) (ACTRIIA).
 GN ACVR2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 NCBI_TaxID=9606;
 (1)
 RP SEQUENCE FROM N.A.
 RC TISSUE-Testis;
 RX MEDLINE=92182002; PubMed=1311955;
 RA Matzuk M.W., Bradley A.;
 RT "Cloning of the human activin receptor cDNA reveals high evolutionary
 RT conservation.";
 RL Biochim. Biophys. Acta 1130:105-108(1992).
 (2)
 RP SEQUENCE FROM N.A.
 RC TISSUE-Testis;
 RX MEDLINE=92331944; PubMed=1314589;
 RA Donaldson C.J., Mathews L.S., Vale W.W.;
 RT "Molecular cloning and binding properties of the human type II
 RT activin receptor.";
 RL Biochem. Biophys. Res. Commun. 184:310-316(1992).
 (3)
 RP SEQUENCE FROM N.A.
 RC TISSUE-Mammary gland;
 RA Geisler A.G.;
 RT Submitted (DEC-1991) to the EMBL/GenBank/DBJ databases.
 (4)
 RP SEQUENCE FROM N.A.
 RA Timmra T., Oida S.;
 RL Submitted (NOV-1994) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: RECEPTOR FOR ACTIVIN A, ACTIVIN B, AND INHIBIN A.
 CC INVOLVED IN TRANSMEMBRANE SIGNALING.
 CC -1- CATALYTIC ACTIVITY: ATP + a protein -> ADP + a phosphoprotein.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC TGFB RECEPTOR SUBFAMILY.
 CC
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 CC
 CC EMBL, X63128; CAA44839.1; -
 CC EMBL, X62381; CAA44245.1; -
 CC EMBL, M93415; AAA5504.1; -
 CC EMBL, D31770; BAA06548.1; -
 CC PIR, S18908; S18908.
 CC PIR, J01486; J01486.
 CC PIR, S22345; S22345.
 CC HSP, P27038; IRYE.
 CC NIM, I02581; -
 CC InterPro, IPR000333; ActivinII_receptor.
 CC InterPro, IPR000472; Activin_rec.
 CC InterPro, IPR000719; Euk_kinase.
 CC InterPro, IPR002290; Ser_thr_kinase.
 CC Pfam, PF01064; Activin_rec; 1.
 CC Pfam, PF00069; pkinase; 1.
 CC PRINTS, PR00653; ACTIVINR.
 CC PROSITE, PS00107; PROTEIN_KINASE_ATP, FALSE_NEG.
 CC PROSITE, PS00108; PROTEIN_KINASE_ST, 1.
 CC PROSITE, PS00111; PROTEIN_KINASE_DOM, 1.
 CC Receptor; Transferase; Serine/threonine-protein kinase; ATP-binding;
 CC Transmembrane; Glycoprotein; Signal.
 CC SIGNAL 1 19
 CC CHAIN 20 513
 CC DOMAIN 20 135
 CC EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 136 161 POTENTIAL.
 FT DOMAIN 162 513 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 192 485 PROTEIN KINASE.
 FT NP_BIND 198 206 ATP (BY SIMILARITY).
 FT BINDING 219 219 ATP (BY SIMILARITY).
 FT ACT_SITE 322 322 BY SIMILARITY.
 FT CARBOHYD 43 43 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 66 66 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CONFLICT 13 13 L -> V (IN REF. 4).
 FT CONFLICT 204 206 GCY -> PSL (IN REF. 4).
 FT CONFLICT 348 348 E -> V (IN REF. 4).
 SQ SEQUENCE 513 AA; 57847 MW; A89822E80979618 CRC64;
 Query Match 10.5%; Score 290.5; DB 1; Length 513;
 Best Local Similarity 29.5%; Pred. No. 6.5e-11;
 Matches 97; Conservative 57; Mismatches 126; Indels 49; Gaps 14;
 QY 12 PAPVLSIELENGELVGRFGTVFAORRRKRGYDAVKIV-----NSRAISREYKAAAS 66
 DB 183 PSLPLGLKPLQLLEEVANRGRFCVWKAO--LLNETYAVKIFPIODQSDQNDNEYVYSLPG 240
 QY 67 LDNEFVRLRGVLEKVMQDPKPAVYTKFMENGLSGLQSCPPRPPLCLRLKEVYL 126
 DB 241 MKHENILQFIQA-EKRGTSVDYDLMLITAFHEKGLSDFLKAVV-SMNELCRIATETMAR 298
 QY 127 GMFYLD-----QNPVLRDLKPSNVLPDELVKLVADFGLS-TEQGGSGSGTSG 177
 DB 299 GLAYLHEDIPGLDGHKPAISHRDIKSNVLLKNNLPACIADGLAKFKREAGKSADGTG 358
 QY 178 EPGGTGLTYLPLPFL--VVNKRKASTASDYSGIIMVNLAGR-----E 219
 DB 359 QV-GTRRRMAPLEVALGALRNDARLRIQMTAMGLVME-LASRCIADGPDVETMLPFE 416
 QY 220 VELPTEPL--VYEAVCNQRNRPISLAPQGPETPGLBGLKELMQLCSSPKRDPSTQ 277
 DB 417 EELQHSRLDQMEVYVHKRRKRPVLRDYMQ---KHAGNAIETIEECMDHAEARLS-A 472
 QY 278 ECLPRTVEFQVHNNNNNAVSTVDFLS 306
 DB 473 GCGVERITOMORLTN-----ITTEDIVT 496
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 ID AVR2_MOUSE STANDARD; PRT; 513 AA.
 AC P27038;
 DT 01-AUG-1992 (rel. 23, Created)
 DT 01-AUG-1992 (rel. 23, Last sequence update)
 DT 16-OCT-2001 (rel. 40, Last annotation update)
 DE Activin receptor type II precursor (EC 2.7.1.37) (ACTR-II).
 GN ACVR2 OR ACVR2A.
 OS Mus musculus (mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 (1)
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91256317; PubMed=1646080;
 RA Mathews L.S., Vale W.W.;
 RT "Expression cloning of an activin receptor, a predicted transmembrane
 RT serine kinase.";
 RL Cell 65:973-982(1991).
 (2)
 RN RAY CRYSTALLOGRAPHY (1.5 ANGSTROMS) OF 25-121.
 RX MEDLINE=99101377; PubMed=9886286;
 RA Greenwald J., Fischer W.H., Vale W.W., Choe S.;
 RT "Three-finger toxin fold for the extracellular ligand-binding domain
 RT of the type II activin receptor serine kinase.";
 RL Net. Struct. Biol. 6:18-22(1999).
 CC -1- FUNCTION: RECEPTOR FOR ACTIVIN A, ACTIVIN B, AND INHIBIN A.
 CC INVOLVED IN TRANSMEMBRANE SIGNALING.
 CC -1- CATALYTIC ACTIVITY: ATP + a protein -> ADP + a phosphoprotein.

CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- TISSUE SPECIFICITY: BRAIN, TESTIS, INTESTINE, LIVER, AND KIDNEY.
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC TGF RECEPTOR SUBFAMILY.
 CC This SWISS-PROT entry is copyright: It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: M65287; AAA37171.1; -
 DR PIR: A39896; A39896.
 DR PDB: 1BTE; 09-FEB-99.
 DR MGI: 102806; Acvrt2.
 DR InterPro: IPR000333; ActivinII_receptor.
 DR InterPro: IPR000472; Activin_rec.
 DR InterPro: IPR000119; Euk_pkinase.
 DR InterPro: IPR002290; Ser_thr_pkinase.
 DR Pfam: PF01064; Activin_resp. 1.
 DR Pfam: PF00069; Pkinase. 1.
 DR PRINTS: PR00653; ACTV1N2R.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; FALSE_NEG.
 DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
 DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
 DR Receptor: Transferrase; Serine/threonine-protein kinase; ATP-binding;
 KM Transmembrane; Glycoprotein; Signal; 3D-structure.
 FT SIGNAL 1 19
 FT CHAIN 20 513
 FT DOMAIN 20 135
 FT TRANSMEM 136 161
 FT DOMAIN 162 513
 FT DOMAIN 192 485
 FT NP_BIND 198 206
 FT BINDING 219 219
 FT ACT_SITE 322 322
 FT CARBOHYD 43 43
 FT CARBOHYD 66 66
 FT SEQUENCE 513 AA; 57889 MW; 475CD292506BAC61 CRC64;
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 Query Match 10.5%; Score 290.5; DB 1; Length 513;
 Best Local Similarity 29.5%; Pred. No. 6.5e-11;
 Matches 97; Conservative 57; Mismatches 126; Indels 49; Gaps 14;
 QY 12 PAPVSTIELENOELVGGGFGVFRRAOHRKMGYDAVKIV-----NSFAISREYKAMAS 66
 DB 183 PSLPLKLEQLDLEVKARGRCQWKAQ--LLNEVAVKIFPIQDRQSMONEYEYVSLPG 240
 QY 67 LDNEFYLRLEGVIERVNDODPKPALVTKRENGSLGSLQSCRPAPPLCRLLEKVEVL 126
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 QY 127 GMFYLD-----ONVYLHRLKPSNVLPDELPYTKADGSL-TOGSGSGTSG 177
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 QY 178 EPGGTIGYAPLPLF---VNVNRKASTADYVSGCITLMAVLAQR-----E 219
 DB 359 QV-GTIRYAPFVLEGCALNFORDAFRLIDYKAMGLVME-LASRCTYADGPDVEYLPFE 416
 QY 220 VELLPEPST--VYEAIVCRONRPSLAEPLQAGPETPGLLEGKLEKMLQICSSPKRPSFQ 277
 DB 417 EEIGQPSLEDNQEVYVVKRRKRPVLRDYO---KHAGNMLCTIEECCHDAEARLS-A 472
 QY 278 ECLPKTDEVFOVVENNMAAVSTYKDFLS 306
 DB 473 GCYGERITOMORITN-----ITTEDIVT 496
 RESULT 14

M3K9_HUMAN
 ID M3K9_HUMAN STANDARD; PRT; 394 AA.
 AC P80192;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Mitogen-activated protein kinase kinase kinase 9 (EC 2.7.1.1-) (Mixed
 DE kinase kinase 1) (Fragment).
 GN MAP3K9 OR MKL1 OR PRKEL.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_Taxid:9606;
 RX MEDLINE:93238756; PubMed:8477742;
 RA DOROV D.S., DEVEREUX L., DIETZSCH E., DE KRETSER T.,
 RT Identification of a new family of human epithelial protein kinases
 RT containing two leucine/isoleucine-zipper domains. J.
 RT Eur. J. Biochem. 213:701-710(1993).
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN EPITHELIAL TUMOR CELL LINES OF
 CC COLONIC, BREAST AND OEOPHAGEAL ORIGIN.
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC MAP KINASE KINASE SUBFAMILY.
 DR PIR: S32467; S32467.
 DR PIR: J00229; J00229.
 DR HSP: P11362; 1PCK.
 DR MIM: 600136; -
 DR InterPro: IPR000719; Euk_pkinase.
 DR InterPro: IPR002290; Ser_thr_pkinase.
 DR InterPro: IPR001245; Tyr_pkinase.
 DR Pfam: PF00069; Pkinase. 1.
 DR SMART: SM00219; TYRCK. 1.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
 DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
 DR Transferrase; Serine/threonine-protein kinase; Tyrosine-protein kinase;
 KM ATP-binding.
 FT NP_BIND 9 17
 FT BINDING 30 30
 FT ACT_SITE 127 127
 FT DOMAIN 127 310
 FT DOMAIN 324 345
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 FT SEQUENCE 394 AA; 44975 MW; DBE40B7D31047FD8 CRC64;
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 QY 69 NEFYLRLEGVIERVNDODPKPALVTKRENGSLGSLQSCRPAPPLCRLLEKVEVL 128
 DB 59 HPNITLARGVCLK---EPNLCLYMERARGCPILNRVLSKRIRP-DILVNAVQIARAH 112
 QY 129 FYLIDQNPV-LIHRDLKPSNVLPDELPYTKADGSL-TOGSGSGTSGSGEP 179
 DB 113 NYLDEAIVPIYIHRDKSSNLIILQKVENGDLSNKIKITDFELAR-----EMHRTTKMSA 168
 QY 180 GGTIGYAPLPLFVNVNRK--STADYVSGCITLMAVLAQREYLPPEP-----SLVTEAV 233
 DB 169 AGTAMAPPE---VIRASNEKSGSDVSYGLMELLTG---EVFPRIQDLRAVATGYA 221
 QY 234 CNRONRPSLAEPLQAGPETPGLLEGKLEKMLQICSSPKRPSFQECPLPTDEV-----FQ 288
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217 YArgGluValGluLeuProThrGluProSerLeuValTyrGluAlaValC 234
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301 ValLysAspPheLeuSerGlnLeuLysSerSerAsnArgArgPheSerI 317
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317 eProGluSerGlyGlnGlyLysThrGluLeuLysPheArgArgTrpI 334
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401 ThrSerThrPheArgAsnGlnMetProSerProThrSerThrGlyThrPr 417
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417 oSerProGlyProArgGlyAsnGlnGlyAlaGluArgGlnGlyMetAsn 434
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434 rPserCysArgThrProGluProAsnProValThrGlyArgProLeuVal 450
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451 AsnLleTyrAsnGlySerGlyValGluValGlyAspAsnAsnTyrLeuTh 467

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467 rMetGlnGlnThrAlaLeuProThrTrpGlyLeuAlaProSerGlyL 484
1401 TATGCACACAGACAACTGCTTGGCCACATGGGGCTTGGACCTCGGACA 1450
484 YArgLysGlyLeuGlnHisPheProProProValGlySerGlnGlyPro 500
1451 AGGCGAGGGGCTTGGACAGACCCGCCACAGTACGTTCCCAAGAAAGCCCT 1500
501 LysAspProGluAlaTrpSerArgProGlnGlyTrpTyrAsnHisSerG 517
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517 YLys 518
1551 GAAA 1554

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seq_documentation_block:
? Sequence 2, Application US/09531914
? Patent No. 626/956
? GENERAL INFORMATION:
? APPLICANT: ZENECA Limited
? TITLE OF INVENTION: PROTEIN ACTIVATOR OF APOPTOSIS
? FILE REFERENCE: PHM.70536
? CURRENT APPLICATION NUMBER: US/09/531.914
? PRIOR FILING DATE: 2000-03-21
? PRIOR APPLICATION NUMBER: 09/329,418
? NUMBER OF SEQ. ID NOS: 39
? SOFTWARE: FASTSEQ for Windows Version 3.0
? SEQ ID NO 2
? LENGTH: 1557
? TYPE: DNA
? ORGANISM: Homo sapiens
US-09-531-914-2

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  quality: 2744.00      length: 518
  ratio: 5.328          gaps: 0
  percent similarity: 99.421  percent identity: 99.228

alignment_block:
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1 ATGTGTCGCTCAAGTTATGGCCACGGTGCCCGCCCTTGATGCTC 50
17 rLleGluGluLeuGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 34
51 CATCGAGAACTGAGAACCAAGAGCTGCTGGCAAAAGCCGGTTCGGCA 100
34 hrValPheArgAlaGlnHisArgLysTrpGlyTyrAspValAlaValLys 50
101 CAGTCTCCGGGCGCAACAPAGAAAGTGGGCTACGATGCGCGCTCAAG 150
51 lLeValAsnSerLysAlaLieserArgLysValLysAlaMetAlaSerLe 67
151 ATCGTAACTCGAAGCGGATATCCAGAGAGTCAAGGCCATGCGAACTC 200
67 uAspAsnGluPheValLeuArgLeuGlnGlyValAlaGluLysValAsn 84
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351 TTGGCGGCTGCTGAAAGAGTGGTGGTGGATGTTTACTGACGACACC 400
134 LnaAsnProValLeuLeuHisArgAspLeuLysProSerAsnValLeuPro 150
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151 AsPProGluLeuHisValLysLeuHisAspPheGlyLeuSerThrPheG 167
451 GACCCAGACCTGCACGCTCAAGCTGCGAGATTGGCTGTCCACATTTC 500
167 nglyGlySerGlnSerGlyThrGlySerGlyGlyLeuProGlyLysThrLeu 184
501 GGGAGGCTCACAGTCAAGGACAGGCTCCGGGAGCCAGGGGACCTTGG 550
184 LyrTrpLeuAlaProGluLeuPheValAsnValAsnArgLysAlaSerThr 200
551 GCTACTGTGGCCCGAAGACTGTTGTAACTGAACCGGAGGAGCCCTCC 600
201 AlaSerAspValTyrSerPheGlyLysLeuMetTrpAlaValLeuAlaG 217
601 GCCAGTCACTACAGCTTCGGGAGCTTAATGTGGCAGTCTTGGTGG 650
217 YArgGlyValGluLeuProThrGluProSerLeuValTyrGluAlaValC 234
651 AAGAGAGTGAAGTGGACACGACGACGACGCTGCTGACGACGACGAGT 700
234 YAsnAsnArgLysAsnArgProSerLeuAlaGluLeuProGlnAlaGlyPro 250
701 GCAACAGAGCAAGAACCGGCTCTATGGCTGAGCTGCCCAAGCCGGGCT 750
251 GluThrProGlyLeuGlnGlyLeuLysGlyLeuMetGlnLeuCysTrpSe 267
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267 rSerGluProLysAspArgProSerPheGlnGlyLeuLeuProLysThrA 284
801 CAGTACCCCAAGAGACGACCCCTCTCCAGGAAAGCTTACCAAAAAC 850
284 spGluValPheGlnMetValGluAsnAsnMetAsnAlaAlaValSerThr 300
851 ATGAGGCTTCCAGATGGTGGAGAACAAATGAAATGCTGCTCTCCACG 900
301 ValLysAspPheLeuSerGlnLeuLysSerSerAsnArgArgPheSer11 317
901 GTAAAGGATTCTCTGCTCAGCTCAGGACGACCAATAGAGATTTCTAT 950
317 eProGluSerGlyGlnGlyLysGlyLysGlyLysGlyLysGlyLysGly 334
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334 LegLysAsnGlnHisSerArgAsnAspValMetValSerGluTrpLeuAsn 350
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417 oSerProGlyProArgGlyAsnGlnGlyAlaGluArgGlnGlyMetAsn 434
1251 AAGTCTGAGACCCGAGGAGAAATCAGGGGGCTGAGAGACAGGACGAACT 1300
434 rPserCysArgThrProGluProAsnProValThrGlyArgProLeuVal 450
1301 GGTCTCGAGAGACCCCGGAGCCAAATCCAGTAAAGGAGGAGCCCTCTT 1350
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: Patent No. 6096539
: GENERAL INFORMATION:
: APPLICANT: ZENECA Limited
: TITLE OF INVENTION: PROTEIN ACTIVATOR OF APOPTOSIS
: FILE REFERENCE: PHM.70536
: CURRENT APPLICATION NUMBER: US/09/329,418
: CURRENT FILING DATE: 1999-06-11
: NUMBER OF SEQ ID NOS: 39
: SOFTWARE: FASTSEQ for Windows Version 3.0
: SEQ ID NO 1
: LENGTH: 1873
: TYPE: DNA
: ORGANISM: Homo Sapiens
: US-09-329-418-1

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Quality: 2714.50      Length: 519
Ratio: 5.271          Gaps: 1
Percent Similarity: 99.229  Percent Identity: 98.651

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alignment_block:

US-09-762-491-6 x US-09-329-418-1 ..

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17 rTleGlnGlnLeuGlnAsnGlnGlnLeuValGlyLysAspGlyPheGlyT 34
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215 CATCGAGAACTGAGACAAACGAGAGCTGTCGCAAAAGCCGCTTCGGCA 264
34 hValAlaPheArgAlaGlnHisArgLysTrpGlyTyrAspValAlaValLys 50
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67  uAaPaangIuPheValIleuArgIleuIuGIyValIleGIuIyValAsnT 84
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765  ACAGCCAGTACGTCACAGCTTCGGGATCCCTAATGTGGAGAGTCTTGC 814
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216  AGIYARGGIuValIuIeuProThrGIuProSerIeuValIyTrpIuIAs 233
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815  TGGAGAGAAAGTTGACTTCCAAACGAAACATCACTCTGTGACAGACGAG 864
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233  aIcYAsnArgIuAsnArgProSerIeuAlaGIuIeuProGIuAlaGIy 249
   |||||||
865  TGTGCAACAGGCGAGAACCGGCTTCAATTGGCTGAGCTCCCAAGCCGGC 914
   |||||||
250  ProGIuThrProGIyIeuGIuGIyIleuIySGIuIeuMetGIuIeuCysTr 266
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915  CTTGAGAACTCCCGGCTTAAAGAGACTGAAGAGCTAAATGCAAGCTCTCTG 964
   |||||||
266  pSerSerGIuProLyAspArgProSerPheGIuIuCyIeuProLyST 283
   |||||||
965  GAGCACTGTGAGCCCAAGAGACAGACCTCTCCAGAAATGAGCTTACCAAAA 1014
   |||||||
283  hrAspGIuValPheGIuMetValIuIAsnAsnMetAsnAlaIAlaIAlaSer 299
   |||||||
1015  CTGATGAAGCTTCCAGATGGTGGAGAACAAATGAATGAGCTGCTCTCC 1064
   |||||||
300  ThrValIyAspPheIeuSerGIuIeuIySSerSerAsnAlaArgPheSe 316
   |||||||
1065  ACGGTAAAGGATTTCTGTCTCAGCTCAGAGCAGACCAATAGGAATTTTTC 1114
   |||||||
316  rIleProGIuSerGIyGIuGIyThrGIuMetAspGIyPheArgTr 333
   |||||||
1115  TATCCAGAGTCAGGCCAAGAGGAGCAAGAAATGATGAGCTTTAGAGAA 1164
   |||||||
333  hrIleGIuAsnGIuIAsSerArgAsnAspValIuMetValSerGIuTrIeu 349
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1165  CCAATAGAAACCAAGCACTCTCTAATGATGATGATGTTTCTGAGTGGCTA 1214

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366  oSerIeuThrIyAsrSerArgAlaGIuIuGIuIuValIProGIuAlaT 383
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1265  GAGCTTACCAAGAGAGAGAGGACCAACAAAGAGAGCGGTTCCACAACTT 1314
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383  rPTAlaGIyThrSerSerAspSerPheAlaGIuIuProGIuIuThrPro 399
   |||||||
1315  GGACAGAGGACATCTTCAATTCATGATGAGCCCAACCTCCCAAGACCA 1364
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400  GIuThrSerThrPheArgAsnGIuMetProSerProThrSerThrGIyTh 416
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416  rProSerProGIyProArgIyAsnGIuIuIuAlaGIuIuArgIuIuMet 433
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1565  GACTATGCACACAGCAACTGCTTGCACATGAGGGCTTGGACACTTCGG 1614
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500  ProLyAspProGIuAlaIuIuIuIuIuIuIuIuIuIuIuIuIuIuIu 516
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1665  CCTAAAGATCCTGAAGCCTGAGACAGCCAGCCAGGAGTGTGATATCAT 1714
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516  rGIyIyS 518
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1715  CCGGAAA 1721

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seq_documentation_block:
; Sequence 1, Application US/09531914
; Patent No. 6267956
; GENERAL INFORMATION:
; APPLICANT: ZENECA Limited
; TITLE OF INVENTION: PROTEIN ACTIVATOR OF APOPTOSIS
; FILE REFERENCE: PHM.70536
; CURRENT APPLICATION NUMBER: US/09/531.914
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 09/329,418
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 1073
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-09-531-914-1

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  Quality: 2714.50      Length: 519
  Ratio: 5.271          Gaps: 1
  Percent Similarity: 99.229  Percent Identity: 98.651
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US-09-762-491-6 x US-09-531-914-1 ..

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17 T1LeuGlu1LysGlu1LysGlu1LysGlu1LysGlu1LysGlu1LysGlu1 34
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215 CATGAGGAAGTGGAGAACAGAGAGCTCGCGCAAGCGGGTTCGCA 264
34 hValAlaPheAlaGlnHisArgLysTrpGlyTyrAspValAlaValLys 50
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51 T1LeuAlaSerLysValAlaIleSerArgGluValLysAlaMetAlaSerLe 67
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315 ATCGAAACCTCGAAGCGCATATCCAGCGAGTCAGAACGCCATGCGCAAGTCT 364
67 uAspAlaGluPheValLeuArgLeuGluGlyValT1LeuLysValAsnTrp 84
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365 GGATACGAATCTGCTGCTGCGCTAGAGGGGTTATCGAGAGGTGCGCG 414
84 rp...AspGlnAspProLysProAlaLeuValThrLysPheMetGluAsn 99
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415 GCTGAGCCCAAGATCCCAACCCGCTCTGCTGCTGCTGCTGCTGCTGCTGCT 464
100 GlySerLeuSerGlyLeuLeuGlnSerGlnGlyProArgProTrpProLe 116
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465 GGCTCTCTTGTGGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 514
116 uLeuCyArgLeuLeuLysGluValAlaLeuGlyMetPheTrpLeuHisA 133
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515 CTTTGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 564
133 spGlnAsnProValLeuLeuHisArgAspLeuLysProSerAsnValLeu 149
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150 ProAspProGluLeuHisValLysLeuAlaAspPheGlyLeuSerTrpPh 166
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166 eGlnGlyCylSerGlnSerGlyTrpGlySerGlyLysGluProGlyLysTrp 183
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665 TCAGGGAGGCTCACAGTCAAGGAGGAGGTCGCGGGAGCCAGGGGCAACC 714
183 euGlyTrpLeuAlaProGluLeuPheValAsnValAsnArgLysAlaSer 199
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715 TGGCTACTTGGCCCCGAACTTTCTTAACGTAAACCGAAGGCTCTC 764
200 ThrAlaSerAspValTyrSerPheGlyIleLeuMetTrpAlaValLeuAl 216
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216 agLysArgGluValGluLeuProThrGluProSerLeuValTyrGluAlaV 233
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865 TGTCCAAACAGCAACAGCGCTCTCTTGGCTGAGCTGCCCAAGCGGG 914
250 ProGluThrProGlyLeuGluGlyLeuLysGluLeuMetGlnLeuCyStr 266
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915 CTTAGAGCTCCCGCTTAAAGAGACTGAAGAGCTAAAGAGCTCTCTCTG 964
266 pSerSerGluProLysAspArgProSerPheGlnLysLeuProLysTrp 283
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965 GAGCAGTACAGCCCAAGAGACAGACCTCTCTCCAGGAAGCTTACCAAAA 1014
283 hTrpArgLysValPheGlnMetValGluAsnAsnMetAsnAlaValSer 299
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416 rProSerProGlyProArgGlyAsnGlnGlyAlaGluArgGlnGlyMetA 433
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seq_name: /cgn2_6/ptodata/2/lna/5/_CONB.seq:us-08-444-005-14
seq_documentation_block:
; Sequence 14, Application US/08444005
; Patent No. 5674734
; GENERAL INFORMATION:
; APPLICANT: Leder, Philip
; APPLICANT: Seed, Brian
; APPLICANT: Stanger, Ben L.
; APPLICANT: Lee, Tae-Ho
; APPLICANT: Kim, Emily
; TITLE OF INVENTION: CELL DEATH PROTEIN
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
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STREET: 225 Franklin Street, Suite 3100
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/444,005
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,164
REFERENCE/DOCKET NUMBER: 00383/026001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 2268 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-444-005-14

alignment_scores:

Quality: 445.50 Length: 603
Ratio: 1.442 Gaps: 23
Percent Similarity: 51.244 Percent Identity: 26.202

alignment_block:

US-09-762-491-6 x US-08-444-005-14 ..

Align seg 1/1 to: US-08-444-005-14 from: 1 to: 2268

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132 CTTCGGGAAGGTGCTCTGTGTACACAGAGAGCCATGATGTGTATCC 181
48 LeuValIleValIleAsn.....SerIleAlaIle 57
182 TGAAGAAAGATACACAGAGCCCAACCCGCTGAGTACATGACAGTCTC 231
58 SerArgGluValIleValIleMetAlaSerIleAsnArgIlePheValAla 74
232 TTGGAAAGGGGGAAGATGATGCACAGACTGAGACACAGTCAAGTGGGAA 281
74 GLeuGluGly...ValIleGluValIleAsnTrpAspIleAsnProIleVal 90
282 GCTACGTGGCATCATCATAGAGAGGAGCACTAT..... 315
90 roIleValValThrIlePheMetGluAsnGlySerIleSerGlyLeuLeu 106
316 ..TCGGGGGATGAGTACATGAGAGAGGAGACCTGATCCACCTCTCA 363
107 GlnSerGlnCysArgProTrpProIleLeuCysArgIleLeuIleVal 123
364 AAGACCCAGATAGATGTCCCACTTCATGAAAGAGAGATATATCGTGA 413
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414 GCCCATAGAAAGCATGTCTACTTACATGACAAAGT.....GTGATAC 457
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157 LysLeuAlaAspPheGlyLeuSerThrPheGlnGlySerGln..... 171
508 AAGATAGCCGATCTGTGTGCTTCTTAAGACATGAGCAAACTGAC 557
172 .....SerGlyThrGlySerGly 178
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178 LysProGlyIleThrLeuGlyIleValAlaProGluLeuPheValIleVal 194
608 ACNAGGTGTATCCCTTACTACATGACAGCCCAACCTGATATGACATC 657
195 AsnArgIleValIleSerThrIleAspValIleTrpSerPheGlyIleLeu 211
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708 TTGGCAATATTTCCAAAAGAGAG.....CCCTATGAG..... 741
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253 GGIleGluGlyLeuIleGluLeuMetGlnLeuGlyTrpSerSerGlu 270
832 .....ATCATGAGCTCATGAGAGAGAGAGAGAGAGAGAGAGAGAG 868
270 IolysAspArgProSerPhe.....GlnGluCysLeuProIle 282
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298 IserThrValIleAspPheLeuSerGlnLeuIleYserSerAsnArgArg 315
960 AAGTTTAAAGAAAGATATCCAGATCAAAGCCAGTGTGTGAGAGATGT 1009
315 heSer.....IleProGluSer..... 320
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321 .....GlyGlnGlyGly 325
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: Sequence 257, Application US/09188930A
: Patent No. 6150502
: GENERAL INFORMATION:
: APPLICANT: Watson, James D.
: APPLICANT: Strachan, Lorna
: APPLICANT: Sleeman, Matthew
: APPLICANT: Onrust, Rene
: APPLICANT: Muriel, James Greg
: TITLE OF INVENTION: Compositions Isolated From Skin Cells
: FILE REFERENCE: 11000.1011c1
: CURRENT APPLICATION NUMBER: US/09/188.930A
: NUMBER OF SEQ ID NOS: 348
: SOFTWARE: FASTSEQ for Windows Version 3.0
: SEQ ID NO 257
: LENGTH: 3516
: TYPE: DNA
: ORGANISM: Mouse
: US-09-188-930-257

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		Percent Identity: 27.441

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112 ArgProTrpProLeuLeuGlyArgLeuLeuGlyGluValAlaLeuGlyMe 128
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834 AGAAATTAATCTCTGTAACAGAGAGCTTTGTGTGAGAAAGCTCATGAGAG 882

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seq_documentation_block:

Patent No. 6211337

APPLICANT: BAICHWA

APPLICANT: HSU, HA

TITLE OF INVENTION:

TITLE OF INVENTION:

CORRESPONDENCE ADDRESS:

STREET: 75 DENIS

CALL: HILLSBORO
STATE: CALIFORNIA

COUNTRY: USA
ZIP: 94010

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; COMPUTER READABLE FILE
; MEDIUM TYPE: FLOPPY

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COMPUTER: IBM PC  
OPERATING SYSTEM:
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; SOFTWARE: Patent
; CURRENT APPLICATION:

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APPLICATION NUMBER:

CLASSIFICATION:
ATTORNEY/AGENT INFO

NAME: OSMAN, RICHARD
REGISTRATION NUMBER

REFERENCE/DOCKET
; RECOMMENDATION T

TELEPHONE: (650) 345-1234

; INFORMATION FOR SEQ I

LENGTH: 2016 bas

STRANDEDNESS: do

MOLECULE TYPE: CDN ;

NAME/KEY: CDS

US-09-132-118-1

quality: 42

Ratio:	1:
Percent Similarity:	50

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33 y1nrvalpneargal ::

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45Tyraspaala

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seq.documentation_block:
Sequence 1, Application US/09132118
Patent No. 6211337
GENERAL INFORMATION:
APPLICANT: BAICHMAL, VIJAY R
APPLICANT: HUANG, JIANING
APPLICANT: HSU, HAILING
TITLE OF INVENTION: RIP: NOVEL HUMAN PROTEIN INVOLVED IN
TITLE OF INVENTION: TUMOR NECROSIS FACTOR SIGNAL TRANSDUCTION, AND SCREENING
TITLE OF INVENTION: ASSAYS
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESS: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 75 DENISE DRIVE
CITY: HILLSBOROUGH
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94010
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/132,118
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A.
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: 795-006-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 343-4341
TELEFAX: (650) 343-4342
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2016 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..2013
US-09-132-118-1

Alignment_scores:
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Ratio: 1.434 Gaps: 23
Percent similarity: 50.862 Percent identity: 25.862

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Align seg 1/1 to: US-09-132-118-1 from: 1 to: 2016

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seq_documentation_block:

Sequence 16, Application US/08444005

Patent No. 5674734

GENERAL INFORMATION:

APPLICANT: Leder, Philip

APPLICANT: Seed, Brian

APPLICANT: Stanger, Ben Z.

APPLICANT: Lee, Tae-Ho

APPLICANT: Kim, Emily

TITLE OF INVENTION: CELL DEATH PROTEIN

NUMBER OF SEQUENCES: 35

CORRESPONDENCE ADDRESS:

ADDRESSEE: Fish & Richardson P.C.


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? sequence 1, application US/09161443A
? Patent No. 6020198
? GENERAL INFORMATION:
? APPLICANT: C. Frank Bennett
? APPLICANT: Lex M. Cowsett
? TITLE OF INVENTION: ANTISENSE MODULATION OF RIP-1 EXPRESSION
? FILE REFERENCE: RTS-0011
? CURRENT APPLICATION NUMBER: US/09/161.443A
? NUMBER OF SEQ ID NOS: 47
? SEQ ID NO 1
? LENGTH: 2617
? TYPE: DNA
? ORGANISM: Homo sapiens
? FEATURE:
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? LOCATION: (1)..(2016)
? FEATURE:
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? LOCATION: 2452
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? NAME/KEY: unsure
? LOCATION: 2496
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US-09-161-443-1

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  Ratio: 1.434        Gaps: 23
  Percent Similarity: 50.862  Percent Identity: 25.862

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33 TyrValPheArgAlaGlnHisArgGlyStrpGly..... 44
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60 GluValLysAlaMetIaSerLeuAspAsnGluPheValIleuArgLeuG1 76
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93 a1ThrLysPheMetGluAsnGlySerLeuSerGlyLeuLeuGlnSerGln 109
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198 AlaSerThrAlaSerAspValTyrSerPheGlyIleLeuMetTrpAlaVal 214
613 CCACACAGAGAGCTCGATGTGATACACTTCTCTGATGATCTGCGCAT 662
214 LLeuValaGlyArgGluValGluLeuProThrGluProSerLeuValTyrG 231
663 ATTTCAAATTAAGAG.....CCATATGA.....A 688
231 LuAlaValCysAsnArgGln.....AsnArg 239
689 ATGCTATCTGTGACACAGCTGTGATTAATGTCAATAATCTGGACAGCG 738
240 ProSerLeuAlaGluLeuProGlnAlaGlyProGluThrProGlyLeuG1 256

```

```

773 CCGATGTGATGATCATCTAGTACCTCCCAAGAGAA..... 777
778 .....
256 uGlyLeuLeuGluLeuMetGlnLeuCysTrpSerSerGluProlyAspA 273
778 .....
273 rGProSerPheGlnGluCysLeuProlyThrAspGluValPheGln... 288
824 GCGCGACATT.....CTCGCATTTAGAAAAAATTTAGCGCT 861
289 .....MetValGluAsnAsnMetAsnAlaValSerThrVa 301
862 TTTTATTATTAAGCTAATAGAAAGAAATGTAGAAAGAGCGTGAAGATT 911
301 LysAspPheLeuSerGlnLeuLysSerSerAsnArgPhe..... 315
912 AAGAAAGAGATTATCAAAACGAAATGCACTGTGAAAGAAATCAGTCTC 961
316 .....SerLeProGluSer..... 320
962 TTCAACTGATTGTGTGGAGTACCTCAAGCGGTCAAAATTCAGCCCA 1011
321 .....GlyGlnGlyGlyTh 325
1012 GAACAGCTGTCTCACTGACACTCCAGAGCTGGAGTGGTCTCTCTGT 1061
325 rGluMetAspGlyPheArgArgThrIleGluAsnGlnIleSerArgAsnA 342
1062 GAGAGAGTCTGGTTGCTCTCTCTCTGAGACACCAAGAGAGAGATG 1111
342 SP.....ValMet 344
1112 AGCCAGCCCTGCAGAGTAACCTCAAGAGCAAGCCAACTACCTTTAT 1161
344 CValSerGluTrpLeuAsnLysLeuAsnLeuGlu..... 355
1162 GCGAGCGCGTGCAGAGCAGAGCAAGCAAGCCAGAGAAATGTGCGC 1211
356 .....GluProProSerSerVal 361
1212 TTACAAAGAGAGAGAGAAAGAGAGAGAGCTCTCCATCACCCTTTTG 1261
362 ProLysLysCysProSerLeuThrLysArgSerArgAlaGlnGluGlu 378
1262 CACAGCAAA.....GACCTTACGAAATTTTCAGAAATTCAGAGGAGAA 1305
378 nVal.....P 380
1306 GCGAGCTGTATTTCAGTGCAGCCAGCTATGCTATCCAGTGCACAGCC 1355
380 rGlnAlaLeuTrpThrAla..... 385
1356 CTCAGGGGCTCACAGCCAACTCAAGTACTGTATCAGAAACAATGATAT 1405
386 .....GlyThrSerSerAspSerMetAlaGlnProProGlnTh 398
1406 ATAGCTCACATGCGCTTTCAGACAGACACTGATCAGCAACAGCAGGT 1455
398 rProGluThrSerThrPheArgAsnGlnMetProSerProThrSerThrG 415
1456 CCGAGAGTTTGTTCAGG.....CCAATTCCAAGTC 1486
415 LysThrProSer.....ProGlyProArgGlyAsnGlnGlyAla 427
1487 ATATGCGTACGTGCATATATATCCAGTGGCTGAGAACCAATATATCA 1536
428 GluArgGlnGlyMetAsnTrpSerCysArgThrProGluProAsnProVa 444
1537 AATTCACCCACATGCCATTCAGCTCTTCCACCCACAGATGAATGTAT 1586
444 LTrnGlyArgProLeuValAsnIleTyraAsnCysSerGlyValGlnValG 461

```

```

1587 AAAA.....TATACATATACAAATAGTACTGCGATTGCATTC 1624
461 LysAspAsnAsnTyrlLeuThrMetGlnGlnThrThrAla 473
1625 GAGCTTACAAATATATATGAGATTGTGTGGAGCAGATTC 1662
seq_name: /cgn2_6/prodata/2/lna/6b_COMB_seq:us-09-133-944-2
seq_documentation_block:
/ Sequence 2, Application US/09133944
/ Patent No. 6280937
/ GENERAL INFORMATION:
/ APPLICANT: Luo, Ting
/ APPLICANT: Luo, Pei Wen
/ TITLE OF INVENTION: SHUTTLE VECTORS
/ FILE REFERENCE: A66252/DJB/DAY
/ CURRENT APPLICATION NUMBER: US/09/133,944
/ EARLIER APPLICATION NUMBER: 09/133,949
/ NUMBER OF SEQ ID NOS: 39
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 2
/ LENGTH: 9687
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: constructed
US-09-133-944-2

alignment_scores:
Quality: 412.00 Length: 580
Ratio: 1.357 Gaps: 23
Percent Similarity: 50.862 Percent Identity: 25.862
alignment_block:
US-09-762-491-6 x US-09-133-944-2 ..
Align seg 1/1 to: US-09-133-944-2 from: 1 to: 9687

17 SerIleGluGluLeuGluAsnGlnGluValGlyLysAspGlyPheG 33
1170 TCCAGTGACTTCTCTGGAGAGTGCAGAACTG...GACAGCGAGCGCTTGG 1216
33 YThrValPheArgAlaGlnIleAsnArgLysTrpGly..... 44
1217 GAAGGTGTCTGTGTGTCCACAGAACCCAGGAGCTCATGATCATGAAAA 1266
45 ....TyraPvalAlaValLysIleValAsnSerLysAlaIleSerArg 59
1267 CAGTGTACAGAGGCGCCCACTGCATTTGAGCACACAGAGCCCTTGGAG 1316
60 GluValLysAlaMetAlaSerLeuAspAsnGluPheValLeuArgLeuCl 76
1317 GAGGCGAAAGATGATGAACAGACTGAGACACAGCCGGGTGTGAAGCTCT 1366
76 uGlyValIleGluLysValAsnTrpAspGlnAspProlyGProAlaLeuV 93
1367 GCGCCTCATC.....ATAGAGGAGAGGAGAACTCCTCTGG 1401
93 AlThrPhePheMetGluAsnGlySerLeuSerGlyLeuLeuGlnSerGln 109
1402 TGATGGAGTACATGAGAAAGGCAACCTGATGCACGTCTGAAAGCGAG 1451
110 CysProArgProTrpProLeuLeuCysArgLeuLeuLysGluValValLe 126
1452 ATGAGTACTCCCTTCTGTGAAAGAGATAAATTTGGCAAAATTCATTCA 1501
126 uGlyMetPheTyrlLeuIleAspGlnAsnProValLeuLeuIleAsnArg 143

```



```

24  ngileuvalaiglyasapglypheglythrvalpheargalaglnhisa 41
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
288  GCGGTACCTGAGCGCGCGCTCTGCACTCTGCTCCGCCGCCGCCGCC 337
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
41  rglvtrpglytyraspvalalaivalylevalasn..... 53
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
338  CAGACTGCCGCGCTGCGCGCTGAGCACTGCACATCCACACTCGG 387
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
54  .....serlysalaleaserargluvalylvalametal 65
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
388  CTGCTCCAGCTGAAAGAGAGATGCTTAAAGAGAGCTGAAATTTC 437
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
65  aserleuaspaasncluphevalleuargleugluvalilegluysv 82
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
438  CAAAGCTAGATTGATACATCTTCCCAATTTGCGAATTCATCCATG 487
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
82  alaantpaspclnaspProlyleProalalevalthrlyspheketlu 98
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
488  CTGAATT.....TTGGAAATGTTACTGAAATACATGCCA 522
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
99  AsnclyserserleuSerGlyleuLeuGlnSerGlnCysProAlaGPro 113
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
523  AATGATCATTTAAATGAACCTCCATACAGAAAAGTGAATATCTGAT 572
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
114  ....TTPProleuLeuCyArgleuLeuysgluvalaleuGlymetp 129
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
573  TGCCTTGCCATTGAGATTGATTCATCTCCATGAAATGCCCTGCTGTA 622
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
129  heTyLeuHlaaspGlnaspProvalleuLeuHlaargpLeuyspPro 145
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
623  ATTACCTGCACAAATATGACTCTCTTACTTCATCATGACTGAAAGCT 672
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
146  SeranvalleuProaspProgluLeuHlaValylleuAlaAspPhegl 162
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
673  CAGAAATCTTATGAGCAATGAAATTCATGTAAGATTGCAATTTTGG 722
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
162  yLeuSerThrPhegl.....GlylySerGlnSerGlythrGlySerg 177
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
723  TTTATCAAGTGGCGCATGATGTCCTCTCACAGTCACAGACTACAAAT 772
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
177  LygluPro...GlyGlyThrLeuGlyTyThrLeuAlaProgluLeuPhe 191
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
773  CTGCACCGAAGAGAGCAATATATATATGCACTGCACTGAAACATATGA 822
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
192  ValanValasnArglysaAserThrAlaSeraspvaltyrSerPhegl 208
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
823  CCTGGACAAAATCAAGGGCAGTATCAAGCAGATATATATAGCTATGC 872
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
208  yLleLeuMetTrpAlaValleuAlaGlyArglu...ValGluLeuProT 224
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
873  AGTATCATCATGCGAAGTCTTATCCAGAAAACAGCCTTTGAAAGTCA 922
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
224  hrgluProSerleuValTyrgluAlaValCysasnArgGlnAsnArgPro 240
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
923  CCAATCTCTTGGCAGATATATGATATATGTC...TCACAGGAGATCGACT 969
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
241  SerleuAlaGlu.....LeuProGlnAlaGlyProgluThrProGlyLe 255
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
970  GTTATATATGAAAGAGTTCATAT.....GATATACCGCAACCG 1010
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
255  uGluGlyLeuLeuMetGlnLeuCyArgleuLeuysgluvalilegluys 272
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
1011  AGCAGCTATGATCTCTTATATAGAAAGTGAAGGCGCAAAAATCCAGTG 1060
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
272  spArgProSerPheGlnGluCyaleuProlyspThrAspGluValPhegl 288
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
1061  AAAACCATCTTCTTAAATGTTAAATGAACTGAAACGAGTTTGCA 1110
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
289  MetValGlu.....AsnAsnMetAsnAlaValAserThrValylsAs 303
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
1111  ACATTTGAGAGATAACTTTCTTGAAGCTGTTATTCAGCTAAAGAAAC 1160
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```

```

303  pPheLeuSerGlnLeuysSerser 311
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
1161  AAGTTACGAGAGTCTTCAAGTCC 1185

seq_name: /cgn2_6/prodata/2/1na/6A.CONB.seq:us-09-188-930-66
seq_documentation_block:
/ Sequence 66, Application us/09188930A
/ Patent No. 6150502
/ GENERAL INFORMATION:
/ APPLICANT: Watson, James D.
/ APPLICANT: Strachan, Lorna
/ APPLICANT: Sleeman, Matthew
/ APPLICANT: Onrust, Rene
/ APPLICANT: Murlson, James Greg
/ TITLE OF INVENTION: Compositions isolated from skin cells
/ FILE REFERENCE: 11000.1011C1
/ CURRENT APPLICATION NUMBER: US/09/188,930A
/ NUMBER OF SEQ ID NOS: 348
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 66
/ LENGTH: 1888
/ TYPE: DNA
/ ORGANISM: mouse
/ FEATURE:
/ NAME/KEY: unsure
/ LOCATION: (1690)...(1690)
/ NAME/KEY: unsure
/ LOCATION: (1755)...(1755)
/ NAME/KEY: unsure
/ LOCATION: (1864)...(1864)
US-09-188-930-66

alignment_scores:
Quality: 391.50      length: 498
Ratio: 1.506         gaps: 21
Percent similarity: 52.209   Percent identity: 28.113

alignment_block:
US-09-762-491-6 x US-09-188-930-66 ..

Align seg 1/1 to: US-09-188-930-66 from: 1 to: 1888

20  gluleuGluAasnGlnGluLeuValGlyLyAspGlyPheGlyThrValph 36
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
64  GAATTCGACGCTGGAGAGAGTGGCTCGCGGCTTCGCGCAGGTGA 113
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
36  eArgAlaGlnHlaArglystrpGlytyrAspValAlaValylleVala 53
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
114  CAGGGTGGCCATGTGCACTGGAAAGCTGGCTCGCATCAGTCAAGTCTCGC 163
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
53  snSerLyAlaIleSer.....ArgGluVal 61
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
164  CCGATCTCACGCTGACAGCAGCAAGCAATGCACTCTCGAGGAAGCT 213
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
62  LyAlaMetAlaSerleuAspAasnGluPheValleuArgleuGlnGlyVa 78
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
214  MGAAGATGAGAGATGGCCAGTCCGATTCATCTACTGCTGACGGCAT 263
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
78  lileGluysValasnTrpaspclnaspProlyspProalaleuValthr 95
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
264  ATGC.....CAGAACT...GTGCGCTGTGTCATGG 292
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
95  yspPheMetGluAasnGlySerleuSerGlyleuLeuGlnSerGlnCysPro 111
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
293  AGTACATGAGACAGAGCTCCCTCGAAGACCTGCTGCTCAGAC...CCA 319
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
112  ArgProtpPpProleuLeuCyArgleuLeuysgluvalilegluys 128
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
340  TTGCTTGGACCTGCGCTTTCGATCGATCGACAGAGACCGCGGCAAT 389
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```


CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: FASTEST for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/019,942
FILING DATE: 06-FEB-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: MelkiJohn, Ph.D., Anita L.
REGISTRATION NUMBER: 35,283
REFERENCE/DOCKET NUMBER: 07334/068001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-3070
TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1931 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
IS-09-019-942-2

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Alignment_scores:
    Quality: 379.00    Length: 319
    Ratio: 1.895      Gaps: 11
    Percent Similarity: 62.656    Percent Identity: 31.661

Alignment_block:
US-09-762-91-6 x US-09-019-942-2 ..

Align seg 1/1 to: US-09-019-942-2 from: 1 to: 1931

14 ProLeuValSerIleGluGluLeuGluAaGlnGluLeuValGlyLysAs 30
    ||||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
244 CCACACATTCCTCCATCCACCAAACTGCCGACCTGCGGTACTGAGCGGGG 299
    30 pGlyPheGlyThrValIlePheArgAlaGlnHisArgLysTyrPglyTyrAsp 47
    :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
294 CGCGCTGCGACTGTGTCGTCGCCGCCGCCACGACACTGCCGCTCCAGG 343
    47 aLaIleValIleValIleValAsn.....Ser 54
    ||||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
344 TGCGCGCTGAAGACACTGCACATCCACACTCCGCTGCACACTGAAGA 393
    55 LysAlaIleSerArgGluValIleLysAlaIleMetAlaSerIleuAspAsnGluP 71
    ||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
394 AbGAGATGCTTAAAGAAAGCTGAATTTTACACAAAGCTAGATTAGTA 443
    71 eValIleuArgLeuGlnGluValIleGluLysValaIleAsnTyrAspGlnAsp 88
    :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
444 CATCTCTCCAAATTTGGCAAAATTCATTCAGTGGCTGAGTT..... 483
    88 rGlySerProIleuLeuValThrLysPheMetGluAsnIleSerLeuSerGly 104
    :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
484 ....TTGGCATATCTCTGCAATACACTGCGCAAAAGCATCAATAAGAA 528
    105 LeuLeuGlnSerGlnCysProArgPro.....TyrProLeuLeuGly 118
    ||||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
529 CTCCTACATAGAGAAATGAAATATCCGATCTTCGCTGGCCATTGAGATT 578
    118 sArgLeuLeuGlnGluValValLeuGlnGlyMetPheTyrLeuHisAspGln 135

```


245 LeuProGlnAlaGlyProGluThrProGlyLeuGluGlyLeuLysGluLe 261
||||| :||| :||| :|||
976 TTGCCAATAT.....GATATACCTCAGCGAGCAGCATGATCTCTCT 1016
261 uMetGlnLeuCysTrpSerSerGluProLysAspArgProSerPheGlnG 278
|:|:|:| |:|:|:|:|:| |:|:|:|:|:| :|||:|:|:|:|:|:|:|
1017 AATAGAAAGTGATGGGACAAATCCAGATGAAAGACCATCTTCTTAA 1066
278 LucylLeuProLysThrAspGluValPheGlnMetValGlu.....Asn 292
:|:|:|:| |:|:|:|:|:| |:|:|:|:|:| :|||
1067 AATGTTTAATAGAACTTGAAACAGCTTTTGAGAACATTGAAAGAGATAACT 1116
293 AsnMetAsnAlaAlaValSerThrValLysAspPheLeuSerGlnLeuLy 309
:|:|:|:| |:|:|:|:|:| |:|:|:|:|:| :|||:|:|:|:|:|:|:|
1117 TTCTTGAAAGCTGTATCTCAGCTAAAGAAACAAAGTTACAGAGTGTTC 1166
309 sSerSer 311
:|:|:|:|
1167 AAGTCCC 1173

.

OM of: US-09-762-491-6 to: N.Geneseq.032802.* out_format: pfs

Date: Aug 13, 2002 11:21 PM

About: Results were produced by the GenCore software, version 4.5.

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Command line parameters:

-MODE=framed_p2n.model -DEV=rlh
-O/cgn2.1/USPTO_epool/US09762491/runat.13082002.153858.4890/app-query.fasta.1.583
-DB=N.Geneseq.032802 -QFMT=fastap -SUFFIX=tns -GAPOP=12.000
-GAEXT=4.000 -MINMATCH=0.100 -LOOPCL=0.000 -LOOEXT=0.000
-GAPOP=6.000 -GAEXT=0.050 -XGAPOP=10.000 -XGAEXT=0.500
-DELCP=6.000 -DELCP=7.000 -START=1 -MATRIX=blonsum62
-TRANS=human40.cdl -LIST=45 -DOCALIGN=200 -THR_SCORE=pcr
-THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pfs
-NORM=ext -HEADSIZE=500 -NLEN=0 -MAXLEN=2000000000
-USER=US09762491 -CGEN=1.183 -NCPU=6 -ICPU=3 -LONGLOG
-DEV_TIMOUT=120 -WARN_TIMOUT=30 -NO_ALERT=wait -THREADS=1

Search information block:

Query: US-09-762-491-6
Query length: 519
Database: N.Geneseq.032802.*
Database sequences: 1736436
Database length: 858457221
Search time (sec): 201.680000

Score_list:

Sequnce Stid Orig ZScore EScore Len 1 Documentation
/SID1/gcgdata/hold-geneseq/geneseqn-emb1/NA2000.DAT:AA50788 + 2770.00 2721.73 3.0e-14
/SID1/gcgdata/hold-geneseq/geneseqn-emb1/NA2000.DAT:AA47102 + 2744.00 2696.18 7.9e-14
/SID1/gcgdata/hold-geneseq/geneseqn-emb1/NA2001A.DAT:AAK61313 + 2744.00 2687.79 2.3e-14
/SID1/gcgdata/hold-geneseq/geneseqn-emb1/NA2001A.DAT:AAK94599 + 2737.00 2687.79 2.3e-14
/SID1/gcgdata/hold-geneseq/geneseqn-emb1/NA2000.DAT:AAK56575 + 2718.00 2668.01 3.9e-14
/SID1/gcgdata/hold-geneseq/geneseqn-emb1/NA2000.DAT:AAK47701 + 2714.50 2665.67 3.9e-14
/SID1/gcgdata/hold-geneseq/geneseqn-emb1/NA2001A.DAT:AAK61312 + 2639.00 2592.29 4.8e-14
/SID1/gcgdata/hold-geneseq/geneseqn-emb1/NA2001A.DAT:AAK28988 + 2639.00 2592.29 4.8e-14
/SID1/gcgdata/hold-geneseq/geneseqn-emb1/NA2001A.DAT:AAK70413 + 2247.50 2200.36 3.2e-14
/SID1/gcgdata/hold-geneseq/geneseqn-emb1/NA2001A.DAT:AAK30546 + 1377.00 1353.55 4.8e-6
/SID1/gcgdata/hold-geneseq/geneseqn-emb1/NA2001A.DAT:AAK57446 + 1194.00 1177.24 3.2e-5
/SID1/gcgdata/hold-geneseq/geneseqn-emb1/NA2001A.DAT:AAK527210 + 1071.50 1056.68 1.6e-5
/SID1/gcgdata/hold-geneseq/geneseqn-emb1/NA2001A.DAT:AAK93320 + 775.50 768.84 1.8e-3
/SID1/gcgdata/hold-geneseq/geneseqn-emb1/NA2001A.DAT:AAK93863 + 775.50 768.84 1.8e-3
/SID1/gcgdata/hold-geneseq/geneseqn-emb1/NA2001A.DAT:AAK47704 + 693.50 694.14 2.6e-3
/SID1/gcgdata/hold-geneseq/geneseqn-emb1/NA2001A.DAT:AAK13974 + 596.00 594.01 9.7e-2
/SID1/gcgdata/hold-geneseq/geneseqn-emb1/NA2001A.DAT:AAK93067 + 596.00 594.01 9.7e-2
/SID1/gcgdata/hold-geneseq/geneseqn-emb1/NA2001A.DAT:AAK527211 + 475.50 474.88 4.2e-1
/SID1/gcgdata/hold-geneseq/geneseqn-emb1/NA2001A.DAT:AAK27526 + 475.50 474.88 4.2e-1
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seq_documentation_block:

ID AA50788 standard; DNA; 1557 BP.

AA50788:

31-MAY-2000 (first entry)

Human Apop3 DNA.

Apop3 protein; apoptotic protein; apoptosis modulation; immunotherapy;
apoptosis-mediated disorder; cancer; autoimmune disorder; cytostatic;
degenerative disorder; viral infection; cell loss;
inhibitor of apoptosis protein; IAP; ss.

Homo sapiens.

Key 1.1557 Location/Qualifiers
CDS /tag= B /product= "Apop3 protein" /transl_except= (pos: 1555..1557, aa: GLX)

WO200007545-A2.

17-FEB-2000.

06-ADC-1999; 99WO-US17776.

06-ADC-1998; 98US-0095587.

06-Aug-1998; 98US-0095590.

08-SEP-1998; 98US-0099486.

(RIGF-) RIGEL PHARM INC.

Luo Y, Huang BCB, Shen M, Yu PW;

WPI: 2000-205547/18.

P-PSDB: AAY45042.

Novel apoptotic proteins Apop1, Apop2 and Apop3 and recombinant nucleic acids encoding them for use in screening modulators which is useful for diagnosis and treatment of diseases

Claim 2; Fig 5; 64pp; English.

The patent discloses the use of novel apoptotic proteins and related molecules involved in apoptosis modulation. Expression vectors comprising the Apop DNA can be used to transform host cells. Apop DNA can be administered as DNA vaccines. Apop proteins are used to make polyclonal and monoclonal antibodies for use in immunotherapy. The proteins are useful in treating apoptosis-mediated disorders including cancer, autoimmune disorders, sustained viral infection, inappropriate cell loss and degenerative disorders. Drug candidates that affect Apop bioactivity are identified by screening. The present sequence encodes Apop3 protein. This was identified using RFP (receptor-interacting protein) as the bait protein employing the yeast two-hybrid screening system. Human Apop3 is expressed in heart, liver, pancreas, placenta, and lung. Overexpression of Apop3 inhibits TNF (tumour necrosis factor) alpha-induced caspase activation without affecting TNFalpha-induced NFkappa B activation.

Sequence 1557 BP; 397 A; 424 C; 446 G; 290 T; 0 other:

alignment_scores:

Quality: 2770.00 Length: 518
 Ratio: 5.347 Gaps: 0
 Percent Similarity: 100.000 Percent Identity: 100.000

Alignment block:

US-09-762-491-6 x AA250788 ..

Align seg 1/1 to: AA250788 from: 1 to: 1557

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 DT 08-NOV-2000 (first entry)
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AC AAA75675;
XX
DT 22-JAN-2001 (first entry)
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XX DNA encoding a human regulator of intracellular phosphorylation.
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 KW neurological disorder; Parkinson's disease; demyelinating disease;
 KW meningitis; developmental disorder; neuromuscular disorder; cancer;
 KW myasthenia gravis; cell proliferative disorder; actinic keratosis;
 KW arteriosclerosis; atherosclerosis; leukemia; melanoma; bronchitis;
 KW autoimmune disorder; inflammatory disorder; Addison's disease;
 KW acquired immunodeficiency disease; allergy; diabetes mellitus;
 KW rheumatoid arthritis; microbial infection; trauma; ss.
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 PE
 XX 18-MAR-1999; 99US-0125593.
 PR 20-MAY-1999; 99US-0135045.
 PR 09-JUL-1999; 99US-0143188.
 XX
 PA (INCYTE) INCYTE PHARM INC.
 PI Bandman O, Tang YT, Yue H, Hillman JL, Baughn MR, Azimzal Y;
 PI Lu DM, Au-Yang J;
 XX WPI: 2000-602121/57.
 DR P-PSDB; AAB18658.
 XX
 XX Novel human intracellular phosphorylation regulator polypeptides and
 PT polynucleotides for diagnosis, prevention and treatment of
 FT neurological, cell proliferative and autoimmune/inflammatory disorders
 FT
 PS
 XX Claim 4: Page 88-89; 96pp; English.
 CC The present sequence encodes a human regulator of intracellular
 CC phosphorylation (HRIP). HRIP is useful for screening agonists and
 CC antagonists of HRIP polypeptide. HRIP and its agonist or antagonist
 CC are useful for treating a disease or condition associated with
 CC decreased or increased expression of functional HRIP. Diseases treated
 CC or diagnosed include neurological disorders such as stroke, Parkinson's
 CC disease, demyelinating diseases, bacterial and viral meningitis and
 CC other developmental disorders of the central nervous system,
 CC neuromuscular disorders, myasthenia gravis, cell proliferative disorders
 CC such as actinic keratosis, arteriosclerosis, atherosclerosis and cancer
 CC including leukemia, melanoma, myeloma and cancer of the adrenal gland,
 CC bladder, bone, bone marrow, liver, lung, muscle, ovary, autoimmune/
 CC inflammatory disorder such as Addison's disease, acquired
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 CC rheumatoid arthritis, microbial infection and trauma.
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Alignment scores:
 Quality: 2718.00 Length: 562
 Ratio: 5.267 Gaps: 1
 Percent Similarity: 91.815 Percent Identity: 91.637

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 US-09-762-491-6 x AAA75675 ..
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457 GlyValGlnValGlyAspAsnAsnTrpLeuThrMetGlnGlnThrAl 473
1664 GGGGTGCAAGTTGAGACAACTACTGACTATGCAAGACAGACACTGC 1713
473 aLauProThrTrpGlyLeuAlaProSerGlyArgGlyArgGlnGln 490
1714 CTGGCCACATGGGGCTTGACACTTCGGGCAAGGGGAGGGGCTTGAC 1763
490 LuProProProValGlySerGlnGluGlyProLysAspProGluAla 506
1764 ACCCCACACAGTACGTTGCAAGAAAGCCCTTAAAGATCTCGAAGC 1813
507 SerArgProGlnGlyTrpTrpAsnHisSerGlyLys 518
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seq_name: /sids1/gcysdata/hold-geneseq/geneseqn-emb1/NA2000.DAT:AAA47701
seq_documentation_block:
ID AAA47701 standard; cDNA; 1873 bp.
XX
XX AAA47701:
XX
XX 08-NOV-2000 (first entry)
XX
XX Kinase of death (KOD) coding sequence.
DE

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XX
XX KOD: Kinase of death; programmed cell death; apoptosis; cancer;
XX autoimmune disease; stroke; Alzheimer's disease; identification; ds.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX CDS 165..1724
XX FT /*tag= a
XX FT /product= Kinase of death
XX
XX US6096539-A.
XX
XX PD 01-AUG-2000.
XX
XX PF 10-JUN-1999; 99US-0329418.
XX
XX PR 10-JUN-1999; 99US-0329418.
XX
XX (ZENNE ) ZENNECA LTD.
XX
XX PA Gomes BC, Prosser JC, Kasof GM;
XX
XX PI
XX
XX DR WPI: 2000-523872/47.
XX
XX PT P-PSDB: AAB01524.
XX
XX PT New nucleic acids encoding a protein activator of apoptosis for
XX PT preventing, diagnosing and treating pathophysiological disorders
XX PT related to apoptosis
XX
XX PS Claim 9; Columns 29-32; 32pp; English.
XX
XX CC The kinase of death (KOD) polypeptide is integral to the activation
XX CC process of cellular apoptosis (programmed cell death). Apoptosis is
XX CC needed to orchestrate biological maintenance of an organism during
XX CC development as well as to preserve the normal function and fitness of
XX CC tissues during a normal life span. Physiological conditions which
XX CC result from aberrant apoptosis may be dire. Cancer and autoimmune
XX CC disease may result when there is too little apoptosis as well as
XX CC severe stroke damage or the neurodegeneration of Alzheimer's disease
XX CC when there is too much apoptosis. The KOD polypeptide is useful for
XX CC studying pathophysiological disorders related to apoptosis as well
XX CC as for identifying compounds that modulate biological and/or
XX CC pharmacological activity of the native mediator of apoptosis.
XX
XX SQ Sequence 1873 bp; 471 A; 531 C; 518 G; 353 T; 0 other:
XX
XX
XX alignment_scores:
XX Quality: 2714.50 Length: 519
XX Ratio: 5.271 Gaps: 1
XX Percent Similarity: 99.229 Percent Identity: 98.651
XX
XX alignment_block:
XX US-09-762-491-6 x AAA47701 ..
XX
XX Align seg 1/1 to: AAA47701 from: 1 to: 1873
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XX 17 TllegGlnGluGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 34
XX 215 CATCGAGAACTGAGAACCCAGAGCTCTGCGCAAGCGCGGTTCGCA 264
XX 34 hValPheArgAlaGlnHisArgGlyTrpGlyTrpAspValAlaValLys 50
XX 265 CAGTGTTCGGGCGCAACATAGGAAGTGGGCTACGATGCGGCTCAAG 314
XX 51 lIleValAsnSerLysAlaIleSerArgGluValLysAlaMetAlaSer 67
XX 315 ATCGTAAATCTGAAAGCGAGATTCAGAGGAGCTCAAGGCCATGCGAGTCT 364

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67 uAAspAnGluPheValLeuAhrGLeuGluGlyValIleGluLysValAsn 84
68 GATTAACGAATTCGTGCTGCGCTCAGAGAGGGGTATCGAGAGGGTCGGCG 414
84 rp... AspGlnAspProValProAlaLeuValThrLysPheMetGluAsn 99
415 GCTGAGGCAAGATCCCAAGCCGGCTCTGCTGATCAATTCATGAGAGAC 464
100 GlysLeuSerGlyLeuLeuGlnSerGlnCysProArgProTyrProLe 116
465 GGCCTCCTGTGGGGCTGTGCTGACGTCCAGTCCCTCGCCCTGCGCGCT 514
116 uLeuGlyLeuLeuLysGluValValLeuGlyMetPheTyrLeuHis 133
515 CTTTGGCCCTGCTGAAAGAGTGGTGTGGATGTTTAACTGACGACG 564
133 spGlnAsnProValLeuLeuHisArgAspLeuLysPProSerHisValLeu 149
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1215 AACAACTGAATCTAGAGAGCTCCACAGCTCTGTTCTAAATAATGCGCC 1264

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1315 GGCACAGAGGACATCTTCATGATTCATGATGATGATGATGATGATGAT 1364
400 GluThrSerThrPheArgAsnGlnMetProSerProThrSerThrGlyTh 416
1365 GAGACCTTACATTCAGAAACAGATGATGATGATGATGATGATGATGAT 1414
416 rProSerProGlyProArgGlyAsnGlnGlyAlaGluArgGlnGlyMet 433
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seq_documentation_block:
ID AAD16312 standard; cDNA; 1873 BP.
XX
AC AAD16312:
XX
DT 19-NOV-2001 (first entry)
XX
DE Human kinase of death (KOD) cDNA.
XX
KW Human; protein activator; apoptosis; kinase of death; KOD; therapy;
cytostatic; ss.
XX
OS Homo sapiens.
XX
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XX
PD 31-JUL-2001.
XX
PF 21-MAR-2000; 2000US-0531914.
XX
PR 10-JUN-1999; 99US-0329418.
XX
PA (ZENE ) ZENCA LTD.
XX
PI Gomes BC, Rasof GK, Prosser JC;

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XX MPI: 2001-535022/59.
DR P-PSDB: AAE09430.

XX New human protein activator protein, useful for treating dysfunctional
PT apoptosis conditions and in screening assays to identify agonists which
PT agonize or mimic biological and/or pharmacological activity -

XX Example 3; Column 29-32; 31pp; English.

XX The invention relates to human protein activator of apoptosis and
CC methods to identify compounds that modulate the biological and/or
CC pharmacological activity of the activator and hence regulate
CC apoptosis. The nucleic acid and amino acid sequences of the kinase
CC of death (KOD) are useful for identifying compounds that modulate
CC the biological and/or pharmacological activity of a native mediator
CC of apoptosis, for treating dysfunctional apoptosis conditions, in
CC screening assays to identify agonists which agonize or mimic
CC biological and/or pharmacological activity, induce production of or
CC prolong the biological half-life of the molecule in vivo or in vitro.
CC The present sequence is a cDNA encoding human KOD protein activator
CC of apoptosis.

XX Sequence 1873 BP; 471 A; 531 C; 518 G; 353 T; 0 other:

alignment_scores: Quality: 2714.50 Length: 519
 Ratio: 5.271 Gaps: 1
Percent Similarity: 99.229 Percent Identity: 98.651

alignment_block:
US-09-762-491-6 x MAD16312 ..

Align seg 1/1 to: MAD16312 from: 1 to: 1873

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465 GGGTCTCTGTGCGGGCTGCTGAGTCCAGTCCCTCGGCGCTGGCGCT 514
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DT 04-APR-2001 (first entry)
XX
DE Human h15590 DNA.
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KW Human; protein kinase; cell growth; tumour; cancer; immune;
KW inflammatory; respiratory; haematological; bone disorder; ds.
XX
OS Homo sapiens.
XX
PN M0200100879-A1.
XX
PD 04-JAN-2001.
XX
PE 30-JUN-2000; 2000MD-DS18291.
XX
PR 30-JUN-1999; 99US-0345473.
PR 01-MAY-2000; 2000US-0562480.
XX
PA (MIL-) MILLENNIUM PHARM INC.
XX
PI Hodge MR, Meyers R, Williamson M.
XX
DR WPI: 2001-061977/07.
XX
PT New protein kinase polypeptides, nucleic acids and anti-kinase
PT antibodies, useful for diagnosing and treating e.g. cancer,
PT inflammatory, immune, cardiovascular and bone disorders -
XX
PS C1alm 1; F1g 10; 93pp; English.
XX
CC The present invention relates to human protein kinase. The proteins
CC are from human genes termed h12832, h14138, h14833, h15990,
CC h15993, h16341 and h2252. The proteins may be used to identify
CC modulators of their activity. The proteins may also be used to derive
CC products for the treatment of cellular growth related disorders,
CC malignancies, cancers, immune, inflammatory, respiratory,
CC haematological and bone-related disorders.
XX
SQ Sequence 1697 BP; 464 A; 451 C; 471 G; 311 T; 0 other;

alignment_scores:
Quality: 2639.00 Length: 497
Ratio: 5.331 Gaps: 0
Percent Similarity: 99.598 Percent Identity: 99.396

alignment_block:
US-09-762-491-6 x AAF29898

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152 GNGCTGCGCTAGAAAGGGTTATCGAGAGGTGAAGTGGAGACCAGATCC 201
88 OLYSPROAlaLeuValThrLysPheMetGluAsnGlySerLeuSerGlyL 105
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138 ULeuHisArgAspLeuLysProSerAsnValLeuProAspProGlnLuh 155
352 CTGCAACCGGACCTCAAGCCATCCAAAGTCTGTCGAGACCAAGAGTGC 401
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AC AAK70413;
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DT 06-NOV-2001 (first entry)
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DE Human Immune/haematopoietic antigen genomic sequence SBO ID NO:25225.
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KW Human; Immune; haematopoietic; Immune/haematopoietic antigen; cancer;
KW cytostatic; gene therapy; vaccine; metastasis; ds.
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OS Homo sapiens.
XX
PN W0200157182-A2.
XX
PD 09-AUG-2001.
XX
PF 17-JAN-2001; 2001WD-US01354.
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PR 31-JAN-2000; 2000US-0179065.

PR 04-FEB-2000; 2000US-0180628.
PR 24-FEB-2000; 2000US-0184664.
PR 02-MAR-2000; 2000US-0186350.
PR 16-MAR-2000; 2000US-0189874.
PR 17-MAR-2000; 2000US-0190076.
PR 18-APR-2000; 2000US-0198123.
PR 19-MAY-2000; 2000US-0205515.
PR 07-JUN-2000; 2000US-0209467.
PR 28-JUN-2000; 2000US-0214886.
PR 30-JUN-2000; 2000US-0215135.
PR 07-JUL-2000; 2000US-0216647.
PR 07-JUL-2000; 2000US-0216880.
PR 11-JUL-2000; 2000US-0217487.
PR 11-JUL-2000; 2000US-0217496.
PR 14-JUL-2000; 2000US-0218290.
PR 26-JUL-2000; 2000US-0220963.
PR 26-JUL-2000; 2000US-0220964.
PR 14-AUG-2000; 2000US-0224518.
PR 14-AUG-2000; 2000US-0224519.
PR 14-AUG-2000; 2000US-0225213.
PR 14-AUG-2000; 2000US-0225214.
PR 14-AUG-2000; 2000US-0225266.
PR 14-AUG-2000; 2000US-0225267.
PR 14-AUG-2000; 2000US-0225268.
PR 14-AUG-2000; 2000US-0225270.
PR 14-AUG-2000; 2000US-0225274.
PR 14-AUG-2000; 2000US-0225275.
PR 14-AUG-2000; 2000US-0225757.
PR 14-AUG-2000; 2000US-0225758.
PR 14-AUG-2000; 2000US-0225759.
PR 18-AUG-2000; 2000US-0226279.
PR 22-AUG-2000; 2000US-0226681.
PR 22-AUG-2000; 2000US-0226686.
PR 22-AUG-2000; 2000US-0227183.
PR 23-AUG-2000; 2000US-0227009.
PR 30-AUG-2000; 2000US-0228924.
PR 01-SEP-2000; 2000US-0228927.
PR 01-SEP-2000; 2000US-0228934.
PR 01-SEP-2000; 2000US-0228934.
PR 01-SEP-2000; 2000US-0228934.
PR 05-SEP-2000; 2000US-0228939.
PR 05-SEP-2000; 2000US-0229510.
PR 06-SEP-2000; 2000US-0230437.
PR 06-SEP-2000; 2000US-0230438.
PR 08-SEP-2000; 2000US-0231242.
PR 08-SEP-2000; 2000US-0231243.
PR 08-SEP-2000; 2000US-0231244.
PR 08-SEP-2000; 2000US-0231413.
PR 08-SEP-2000; 2000US-0231418.
PR 08-SEP-2000; 2000US-0232080.
PR 08-SEP-2000; 2000US-0232081.
PR 12-SEP-2000; 2000US-0233196.
PR 14-SEP-2000; 2000US-0233397.
PR 14-SEP-2000; 2000US-0233398.
PR 14-SEP-2000; 2000US-0233399.
PR 14-SEP-2000; 2000US-0233400.
PR 14-SEP-2000; 2000US-0233401.
PR 14-SEP-2000; 2000US-0233401.
PR 14-SEP-2000; 2000US-0233563.
PR 14-SEP-2000; 2000US-0233564.
PR 14-SEP-2000; 2000US-0233565.
PR 21-SEP-2000; 2000US-0234223.
PR 21-SEP-2000; 2000US-0234274.
PR 25-SEP-2000; 2000US-0234997.
PR 25-SEP-2000; 2000US-0234998.
PR 26-SEP-2000; 2000US-0235484.
PR 27-SEP-2000; 2000US-0235834.
PR 27-SEP-2000; 2000US-0235835.
PR 29-SEP-2000; 2000US-0236327.
PR 29-SEP-2000; 2000US-0236367.
PR 29-SEP-2000; 2000US-0236368.
PR 29-SEP-2000; 2000US-0236369.
PR 29-SEP-2000; 2000US-0236370.
PR 02-OCT-2000; 2000US-0236807.
PR 02-OCT-2000; 2000US-0237037.

Dislclosure: SEQ ID NO 25225; 3071pp + Sequence listing: English.

XX

CC AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (1)

CC amino acid sequences given in AAK62170 to AAK61921. (1) Have cytosolic

CC activity, and can be used in gene therapy and vaccine production. (1)

CC proteins and polynucleotides may be used in the prevention, diagnosis and

CC treatment of diseases associated with inappropriate (1) expression. For

CC example, they may be used to treat disorders associated with decreased

CC expression by rectifying mutations or deletions in a patient's genome

CC that affect the activity of (1) by expressing inactive proteins or to

CC supplement the patients own production of (1). Additionally, (1)

CC polynucleotides may be used to produce the secreted (1), by inserting

CC the nucleic acids into a host cell and culturing the cell to express the

CC protein. (1) proteins and polynucleotides may be used to prevent,

CC cancer and treat immune/haematopoietic-related diseases, especially

CC cancers and cancer metastases of haematopoietic-derived cells. AAK64703

CC to AAK87694 represent human immune/haematopoietic antigen genomic

CC sequences from the present invention. AAK51942 to AAK54950 and AAK62169

CC represent sequences used in the exemplification of the present invention

XX

SO Sequence 3970 BP; 933 A; 1204 C; 1015 G; 818 T; 0 other;

Alignment_scores:

Quality: 2247.50	Length: 1143
Ratio: 4.416	Gaps: 11
Percent Similarity: 44.532	Percent Identity: 44.269

alignment_block:

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Align seg 1/1 to: AAK70413 from: 1 to: 3970

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389 CTCAGGCCCGAGGGGTGCCCCGCCCTTGTCATCGAAGAACTGGA 438

22 uASnGInGluLeuValIGlyLysASPjYpNagLYTTrValIPheATGAlag 39

439 GAACGAGAGACCTGCTCGCCAAAGCGGGGTTCGGCAACAGTCTCCGGCCG 488

39 InHlARgLySTrPcLyTrpAlaAlaValLysIleValAnSer... 54

489 AACATAGGAAGTGGGGGTACGATGTGGGTCAAGATGTAAATCCTGCGA 538

54

539 GTGACCCCGGTTGACCCGACGCGAATCTGGCCAAAGAGTGAGACCTACT 588

54

589 GTGCTGTGGGGCCCTGAATGCGAAGGAGGAGATTTCACACGCCCGCT 638

55

639 GCGAGCTCCAGCTCTCTCTGGAGGTGTAGAAAGGCGCATATCCAGGAGGTC 688

62 LysAlaMetAlaSerLeuASPAnGluPheValLeuArgLeuGluGlyVa 78

689 AAGGCCATGGCAAGTCTGGATACGAATTCGTCTCGCTCGCTGAAAGGGGT 738

78 IILeGluysValAenTPAPGInAApPcLySPcAlaLeuValITpTL 95

739 TATCGAAGAGGTGAACGTGGACACAGATCCCAAGCCGGCTCTGGTGACTA 788

95 ySPheMetGluAnGlySerLeuSerGlyLeuLeuGlnSerGlnCysPro 111

789 AATTCATGGAGAAAGGCTCTTGTTCGGGGGTGTGTGAGTCCAGTGGCT 838

112 ArgPTrIPProLeuLeuCYsArgLeuLeuLysGluValIValLeuGlyme 128

839 CGGCGCTGGCGCTCTCTTGGCGCGCTCTCAAAAGAAAGTGGTGTGGGAT 888

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128 tPheTYrLeuHISAspGlnAspProValLeuLeuHISArgAspLeuLysP 145
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889 GTTTTAACTGCAAGACCAAGAACCCGGTCTCTGCAACGGGACCTCAAGC 938
145 roSerAsnValLeuProAspProGlnLeuHISValLys 157
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939 CATCAACGTCCTGCTGACCCAGAGCTGCAAGTCAAGGTCAAGTGTCT 988
157 ..... 157
989 ACACCCCTTCAGACCTCAAGACAAAGCCCAAGCTCTCCAGCAGCACC 1038
157 ..... 157
1039 CGCCGAGACTAGACTCTCAGACCCCTGTCTATGATAGGCTAGCCCTC 1088
157 ..... 157
1089 TCCTCTGACACAGAGCTGCAAGGAGAACAAAGCCCAAGCAGACTTTTA 1138
157 ..... 157
1139 GCTCTGCTGCAAGAGTGAATAGAGGCCCTGAGCCACAGAGTCAATTGCA 1188
157 ..... 157
1189 CCAAGTCCCCACAGCCCTCCAAAGACTATGCTGACCCAGCCCTGCG 1238
157 ..... 157
1239 AGACTCAGACCTTGACCTAGCCCTTACAGAGCAGCAGTATCTACATC 1288
157 ..... 157
1289 CAAGGAACTCTTCCCTTACCTCCACACACTCCCTTTACAAAGCTGAAC 1338
157 ..... 157
1339 TCACACTTCTGGGGCCAGGGGCTTCTCTGAGGCTCTGGCCCCCTGT 1388
158 ..... LeuHISAspPheGly 162
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1389 CTTCCTACACTCCCACTTCTTCTCTCTTTCAGACTGGCAGATTTTGGC 1438
163 LeuSerThrPheGlnGlySerGlnSerGlyThrGlySerGlyGluPr 179
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179 OGlyGlyThrLeuGlyTYrLeuHISLeuProGlnLeuPheValAsnValAsn 196
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1489 AGGGGGCACCCTGGGCTACTTGGCCCCAGAACGTGTTGTTAACGTAAAC 1538
196 rGlyValAserThrAlaSerAspValTYr 205
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1539 CGAAGGCTCTCACACAGCAGTGAAGCTTACAGGTAAAGATCCCGGCCAAA 1588
205 ..... 205
1589 CACACAGCCAGATTCCTACACTTCTGAGGCCCTCCAGGGGATGATGT 1638
205 ..... 205
1639 ATAGAAAGAGTCTTGCCAGTATGAGACCATCTCAGCTTGTGTGTCT 1688
206 ..... SerPheGlyIleLeuMetTrpAlaValLeuAlaGlyArgGluVal 220
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1689 CTGTCACTTCGGGATCTTAATGTGGGAGTCTGCTGGAAAGAAAGTT 1738
221 GlnLeu 222
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1739 GAGGTAAAGCTAGAGGATTCGTGATCTTAACCCAGAGTCCCTT 1788
222 ..... 222

1789 CTCCTGAAGCCCAAGGCTTCCCTTCCCGCTCACCTACTTAGACTGCC 1838
222 ..... 222
1839 CTCCTCCCTCTGTCGCCCCACATTACACTCCCTGCTCTTTCATGAT 1888
222 ..... 222
1889 GAAGCAGTAATTCCTTTTACCCTGAATGCCTGTCTTCACCTCTCT 1938
223 ..... ProThrGluProSerLeuValTYrGlnAlaValCys 224
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1939 CCCCTACTCCAGTGCACCAAGCAACATCACTGTGTACGAAGCAGTGTGC 1988
235 AsnArgGlnAsnArgProSerLeuAlaGlnLeuProGlnAlaGlyProGln 231
|||||
1989 AACAGCAGAAACCGGCTTCATTGCTGAGCTGCCCCAAAGCCGGGCTGGA 2038
251 uThrProGlyLeuGlnGlyLeuLysGlnLeuMetGlnLeuCYrTrpSer 268
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268 ArgGluProLysAspArgProSerPhe 276
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2089 GTGAGCCCAAGCAGACCTCTCTCCAGGCTGAGCTGGCCAGTTACTGT 2138
276 ..... 276
2139 GATCTAGATAAAGCTGGTCTGTGACAGAGGGCTTTTCTCAGAAAAAG 2188
277 ..... GlnGluCysLeuPr 281
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2189 AAGATTGCTCAGCTGCACCTGCACCTGCTGTGCTCTGATGAAATGCTACC 2238
281 ouLysThrAspGlnValPheGlnMetCysIleGlnAsnAsnMetAsnAlaVal 298
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2239 AAAAAGTATGAAGCTTCCAGATGTGTGAGAAACAATATGATCTCTGTG 2288
298 aLserThr 300
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2289 TCYCCAGGTGAGTGCACACATCACCCCTCCCAAGAGCTGTGACAGGAT 2338
300 ..... 300
2339 GGCACAGGTGCTACTGCGCATCCAAATGACTCACACACTACACACTGCT 2388
300 ..... 300
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300 ..... 300
2439 CCAGACACAGATTATGAGCCGAGACACTACCTCCCTGGCTTACCTGCG 2488
301 ..... ValLysAs 303
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2489 CTCATCCAAATCATACCCAGCAAACTCTCCCATCCCTGCAGAGTAAAGGA 2538
303 PheLeuSerGlnLeuLysSerSerAsnArgArgPheSerIleProGln 320
|||||
2539 TTTTCGTCTCAGCTCAGGAGCAGCAAAATGAGAAATTTCTATCCCAAGT 2588
320 ArgGlnGlnGlyThrGlnMetAspGlyPheArgArgThrIleGlnAsn 336
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2589 CAGGCCAAGAGAGGACAGAAATGATGCTTATGAGAGAACCATGTGAAC 2638
337 GlnHISerArgAsnAspValMetValSerGlnTrpLeuAsnValLeuAs 353
|||||
2639 CAGCACTCTCGTAATGATGTATGATGTCTGAGTGGCTTAACCAAGTGA 2688
353 nLeuGlnLeuProProSerSerValProLysLysProSerLeuThr 370
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2689 TCTAGAGAGACCTCCAGCTCTGTCTCTTCTTAAAAAATCCCGAGCTTACCA 2738
 370 ybatgseratgalainglugluglivalproglinalatpfrthalgly 386
 2739 AGAGGACACGGGCACAGAGGAGCAGCTTCCACAGCCTTGACAGCAGGC 2788
 387 ThseSerApsSerMetAlaGlnProGlnThrProGlnThrSerTh 403
 2789 ACATCTCAATTCGATGAGGGCCCAACTCCCACTCCAGAGACTCAAC 2838
 403 rPhaArAsnGlnMetProSerProThrSerThrGlyThrProSerProG 420
 2839 TTTGAAACCAAGATGCCAGCCCTACCTCAACTGAAACACCAAGTCTTG 2888
 420 lProArgGly..Asn..... 424
 2889 GACCCCGAGGAAATCAGGTGAGCATTCAGAGATTAGGGATGCACATA 2938
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 425 GlnGlyAlaGlnArgGlnGlyMetAspTrpSerGlyArgProG 440
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 440 lUpProAsnProValThr..... 445
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 445 445
 3139 TCAATCTTCCACAGACACTCTCTCCACAGACTATATCTAGATTCAAGGT 3188
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 446 GlyArgProLeuValAsnIleTyrAsnGlyValGlnVal 460
 3589 CTTAAAGGCGACCGCTGTTAACTATACAACTGCTCTGGGGTGCAAGT 3638

460 lclYAspAsnAsnTyrIleuThrMetGlnGlnThrAlaLeuProThrT 477
 3639 TGAGACAAACAACACTACTGACTATGCAACAGACAACTGCTTGGCCACAT 3688
 477 rGlyLeuAlaProSerGlyLysGlyArgGlyLeuGlnHisProPro 493
 3689 GGGGCTTGCACTTCGGGCAAGGGAGGGGCTTGACAGACCCCCACCA 3738
 494 ValGlySerGlnGlnGlyProLysAspProGlnAlaTrpSerArgProG 510
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 510 nGlyTrpTyrAsnHisSerGlyLys 518
 3789 GGGTGTGATATATCATAGCGGAAA 3813
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 seq_documentation_block:
 ID AAF30546 standard; cDNA; 1437 BP.
 AC AAF30546;
 DT 29-MAY-2001 (first entry)
 XX
 DE Rat R1P-3-like death-associated kinase (R3DAK) cDNA.
 XX
 KW R1P-3-like death-associated kinase; R3DAK; rat; antibacterial;
 KW virulence; protozoicide; cardiant; antiinflammatory; vasotrophic;
 KW antidiabetic; antitumor; analgesic; immunosuppressive;
 KW antihydrolid; antilucer; nephrotropic; cytoskeletal; nootropic;
 KW anticonvulsant; hepatotropic; antiallergic; antitoxic;
 KW dermatological; osteopathic; antiarrhythmic; urothelic;
 KW ophthalmological; antiparkinsonian; antiproliferative; neuroprotective;
 KW pulmonary; hormonal; apoptosis; gene therapy; vaccine; ss.
 XX
 OS Rattus sp.
 XX
 PN M0200119990-A1.
 XX
 PD 22-MAR-2001.
 XX
 PF 15-SEP-2000; 2000NC-0525201.
 XX
 PR 17-SEP-1999; 99US-0154422.
 XX
 PA (IMNV) IMMUNEX CORP.
 XX
 PI Virca GD, Bird TA;
 XX
 DR WPI: 2001-244803/75.
 XX
 DR P-PSDB; AAB20345.
 XX
 PT New isolated R1P-3-like-death-associated kinase polypeptide for
 PT treating multiple sclerosis, Parkinson's disease, Sjogren's disease,
 PT infections, tumours, cardiovascular and lymphoproliferative disorders
 XX
 PS Claim 5, Page 56-57, 63pp; English.
 XX
 CC The present sequence is that of the coding region of cDNA encoding
 CC rat R1P-3-like-death-associated kinase (R3DAK, see AAB20345), a
 CC member of the R1P3 family, which is known to be involved in
 CC apoptosis. The cDNA was obtained from a rat dermal papilla cell
 CC library. The invention provides R3DAK polypeptides and
 CC polynucleotides, expression vectors, recombinant host cells, and
 CC methods of producing a recombinant R3DAK polypeptide, as well as
 CC antibodies a method of designating an R3DAK inhibitor on the basis
 CC of the 3-dimensional structure of a R3DAK polypeptide, a method of
 CC identifying compounds that alter R3DAK kinase activity, and for
 CC using such compounds. R3DAK, its fragments, variants, antagonists,
 CC agonists, antibodies and binding partners are useful for treating:
 CC bacterial, viral or protozoal infections; cardiovascular disorders such

CC as myocardial infection, heart failure, or vacuulitis; solid tumours;
 CC chronic pain; endocrine system disorders such as diabetes;
 CC hypochromidism and thyroditis, including Hashimoto's thyroditis;
 CC gastrointestinal diseases such as Crohn's disease and ulcers;
 CC genitourinary system disorders such as glomerulonephritis; hematologic
 CC and oncologic disorders such as cancer; lymphoproliferative disorders
 CC such as Hodgkin's disease; hereditary conditions such as Gaucher's and
 CC Huntington's disease; liver disorders such as hepatitis; non-arthritis
 CC medical conditions of the bones and joints; pulmonary disorders such as
 CC cystic fibrosis; allergies; rheumatic disorders such as systemic lupus
 CC erythematosus, gout, osteoarthritis, Reiter's disease;
 CC graft-versus-host disease; female reproductive system disorders; and
 CC diseases such as multiple sclerosis, Parkinson's disease, Sjogren's
 CC disease. R3DK is useful for effecting bodily characteristics,
 CC diathylums or cardiac cycles or rhythms; effecting the fertility of
 CC male or female subjects; effecting the metabolism, catabolism,
 CC anabolism, processing, utilization, storage or elimination of dietary
 CC fat, lipid, polypeptide, carbohydrates, vitamins, minerals, cofactors
 CC or other nutritional factors or component(s); effecting behavioural
 CC characteristics; providing analgesic effects or other pain reducing
 CC effects; promoting differentiation and growth of embryonic stem cells
 CC in lineages other than haematopoietic lineages; hormonal or endocrine
 CC activity; treatment of hyperproliferative disorders;
 CC immunoglobulin-like activity; and the ability to act as an antigen in a
 CC vaccine composition. Nucleic acids encoding R3DK are useful for
 CC diagnostic purposes, for expressing recombinant polypeptide for
 CC analysis, characterisation or therapeutic use, as markers for tissues
 CC in which the corresponding polypeptide is preferentially expressed,
 CC to compare with endogenous DNA sequences in patients to identify
 CC potential genetic disorders; as an antigen to raise anti-DNA
 CC antibodies or elicit another immune response; and for gene therapy.
 CC
 XX

50 Sequence 1437 BP: 368 A: 359 C: 399 G: 311 T: 0 other:

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 Quality: 1377.00 Length: 490
 Ratio: 3.672 Gaps: 6
 Percent Similarity: 76.531 Percent Identity: 59.796

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16 lSerIleGluIleuGluAsnGlnGluLeuValGlyLysAspLysPheG 33
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51 GGGCTCTGAAGAACTGGAGAACTTGTGGGCAAGCGGGTTCG 100
33 LysThrValPheArgAlaGlnHisArgLysTrpGlyTyrAspValAlaVal 49
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101 GAGCCCTGTTCGGGGCAGCCACACAGCATGGAACCTTGATGTGCGATC 150
50 LysIleValAsnSerLysAlaIleSerArgLysValLysAlaMetLase 66
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151 AAGATGCTGACACGAGAAAGATATCCAGGAGCGAAGCCTATGTCGAA 200
66 rLeuAspAsnGluPheValLeuArgLeuGluGlyValIleGluLysVala 83
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201 TCTTCTCTCTGAGAACGCTGCTCTCTCTGCGGCTCACTGAAACCTTCG 250
83 SerThrAspGlnAspProLysProAlaLeuValThrLysPheMetGluAsn 99
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251 AGTGGGACTACGTGTACGGCCGGCTGTGTGACAGATTCATGAGAAC 300
100 GlySerLeuSerGlyLeuArgLysSerGlnCysProArgProTrpProLe 116
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301 GCGTCCCTCTCAGGGCTGTGCAACCTTCATGCCCTGCGCCCTGCTCT 350

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181 LysThrLeuGlyTyrLeuAlaProGluLeuPheValAsnValAsnArgLys 197
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551 GACACCTGATCTACTTGGCCCAAGACCTGTGGATTAAT...GACGGAA 597
198 AlaSerThrAlaSerAspValLysSerPheGlyIleLeuMetThrAlaVa 214
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598 GCTTCTAAGCAAGTATGTGTACAGTGTGGGCTCTGCTGTGACAGT 647
214 lLeuAlaGlyArgGluValGluLeuProThrGluProSerLeuValTyrG 231
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648 GCTGGCTGGAAGAGAAAGCTGAGGTGATACAAAGCACTAATTCGTG 697
231 LuAlaValCysAsnArgGlnAsnArgProSerLeuAlaGluLeuProGln 247
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698 GAGCAGTGTGTACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 747
248 AlaGlyProGluThrProGlyLeuGluGluLysGluLeuMetClnLe 264
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748 GACACCCCTGAGACTCTGCTTACAGAGACTGAAAGAGTAAATGACCA 797
264 uCysTrpSerSerGluProLysAspArgProSerPheGlnGluCysLeuP 281
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798 TGTCTGAGATCTGAGCCTTAAAGACAGGCATCCTTCAAGACTGTGAAT 847
281 rGlyThrAspGluValPheGlnMetValGluAsnAsnMetAlaAla 297
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848 CAATAACCAATAAATGTTTACATCTGTGACAGCAAGTACAGTCTGCT 897
298 ValSerThrValLysAspPheLeuSerGlnLeuLysSerSerAsnArg 314
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898 GTCTCAAGGTAAAGCATATCTGTCTCAGTACAGAAAGCATGACACAA 947
314 gPheSerIleProGluSerGlyGlnGlyThrGluMetAspGlyPheA 331
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948 GTTGTCTCCAGACAGTCCAGCCAAAGGTCACAGGTGATTCGCCCA 997
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348 TrpLeuAsnLysLeuAsnLeuGluGluProProSerSerValProLys 364
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1018 ATGCTGAGCGCGCTGCATCTGGAGAGCCTTGTGATCAGTCTCTGAAG 1067
364 eCysProSerLeuThrLysArgSerArgAlaGlnGluGlnValProG 381
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1115 ATGCACACACAGCAGGAGATCATCTGACACTTGGCTGACACCTCCCA 1164
398 ThrProGluThrSerThrPheArgAsnGlnMetProSerProThrSer 414
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1165 ATTCACATACATTACCTCCAGACAGCAACACACTAGCCACACTTAC 1214
414 rGlyThrProSerProGlyProArgGlyAsnGlnGlyAlaGluArgGln 431

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744 TGGAGCAGCCACAGGCTGGTATATCATACGGGAAA 782

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seq_documentation_block:

ID AA527210 standard: cDNA, 960 BP.

XX AA527210:

XX 07-NOV-2001 (first entry)

DE cDNA encoding novel signal transduction pathway protein, Seq ID 245.

XX Neuroprotective; cytosolic; dermatological; immunosuppressive; tumour;
 KM antiinflammatory; anti-HIV; antibacterial; antiinflammatory; cancer;
 KM immune system disorder; rheumatoid arthritis; inflammatory condition;
 KM organ transplant rejection; infection; hepatitis C; blood disorder;
 KM sickle cell anemia; hyperproliferative disorder; Gaucher's disease;
 KM neurodegenerative disorder; Alzheimer's disease; Parkinson's disease;
 KM chromosomal abnormality; Down syndrome; leishmaniasis; renal disorder;
 KM cardiovascular; respiratory; wound healing; endocrine; Addison's disease;
 KM reproductive system; gastrointestinal; liver disorder; AIDS; ss;
 KM acquired immune deficiency syndrome.

XX Homo sapiens.

XX MO200154733-A1.

XX 02-AUG-2001.

XX 17-JAN-2001: 2001WO-US01312.

XX 31-JAN-2000: 2000US-0179065.
 PR 04-FEB-2000: 2000US-0180628.
 PR 24-FEB-2000: 2000US-0184664.
 PR 02-MAR-2000: 2000US-0186350.
 PR 16-MAR-2000: 2000US-0189874.
 PR 17-MAR-2000: 2000US-0190076.
 PR 18-APR-2000: 2000US-0198123.
 PR 19-MAY-2000: 2000US-0205515.
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XX Homo sapiens.
OS
XX
PN EP1130094-A2.
XX
PD 05-SEP-2001.
XX
PE 07-JUL-2000; 2000EP-0114089.
XX
PR 08-JUL-1999; 99JP-0194486.
PR 11-JAN-2000; 2000JP-018774.
PR 02-MAY-2000; 2000JP-0183765.
XX
PA (HELI-) HELIX RES INST.
PI Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y;
PI Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;
XX
DR WPI; 2001-524255/58.
XX
PT 830 Primers useful for synthesizing full length cDNA clones and their
PT use in genetic manipulation -
XX
PS Claim 2: SEQ ID NO 780; 1380bp + sequence listing; English.
XX
CC The invention relates to primers for synthesizing full length cDNA
CC clones. 830 cDNA molecules encoding a human protein have been
CC isolated and nucleotide sequences of 5' - and 3' - ends of the cDNA
CC molecules have been determined. Primers for synthesizing the full length
CC cDNA are useful for clarifying the function of the protein encoded by
CC the cDNA. The full length clones were obtained by construction of full
CC length enriched cDNA libraries that were synthesized by the oligo-capping
CC method. The primers enable the production of the full length cDNA easily
CC without any special methods. The present sequence is the nucleotide
CC sequence of the 5' - end of a cDNA provided in the invention.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in CD-ROM format directly from EPO.
XX
SO Sequence 665 BP; 147 A; 194 C; 190 G; 130 T; 4 other;

Alignment scores:
Quality: 775.50 Length: 169
Ratio: 4.847 Gaps: 2
Percent Similarity: 94.675 Percent Identity: 93.491

alignment block:
US-09-762-491-6 x AAK932320 ..

Align beg 1/1 to: AAK932320 from: 1 to: 665

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67 uAspAsnGluPheValLeuArgLeuGlnGlyValIleGluLyValAsn 84
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365 GGATTAAGGAATTCGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 414
84 tPAspGlnAspProLyGProAlaLeuValTyrLysPheMetGlnAnGly 100
|||||

415 GGGACCAAGATCCCAAGCCGCTCTGTGACTAAATTCAATGAGACGCC 464
101 SerLeuSerGIyLeuGlnSerGlnCysProArgProTProLeuLe 117
|||||
465 TCCCTGTGCGGCGCTGCTGAGTCCAGTCCCTCGCCCTCGGACCT 514
117 uCyArgLeuLeuLyGluValValLeuGlyMetPheTyryLeuHlaSp 134
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661 ANGA 665

seq_name: /SIDSI/gcgdata/hold-geneseq/geneseqn-emb1/NA2001A.DAT:AAK93863

seq_documentation_block:

ID AAK93863 standard; cDNA; 665 BP.

XX AAK93863;

XX 06-NOV-2001 (first entry)

DE Human cDNA clone representative sequence, SEQ ID NO: 2323.

XX Human: full length cDNA; cDNA synthesis: oligo-capping; ss.

OS Homo sapiens.

PN EP1130094-A2.

PD 05-SEP-2001.

PE 07-JUL-2000; 2000EP-0114089.

PR 08-JUL-1999; 99JP-0194486.

PR 11-JAN-2000; 2000JP-018774.

PR 02-MAY-2000; 2000JP-0183765.

XX (HELI-) HELIX RES INST.

PI Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y;
PI Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;

DR WPI; 2001-524255/58.

PT 830 Primers useful for synthesizing full length cDNA clones and their
PT use in genetic manipulation -

PS Example 11: SEQ ID NO 3233; 1380bp + sequence listing; English.

XX The invention relates to primers for synthesizing full length cDNA
XX clones. 830 cDNA molecules encoding a human protein have been
XX isolated and nucleotide sequences of 5' - and 3' - ends of the cDNA
XX molecules have been determined. Primers for synthesizing the full length
XX cDNA are useful for clarifying the function of the protein encoded by
XX the cDNA. The full length clones were obtained by construction of full
XX length enriched cDNA libraries that were synthesized by the oligo-capping
XX method. The primers enable the production of the full length cDNA easily
XX without any special methods. The present sequence was used as the
XX representative sequence from a human clone which was used in
XX homology searches to identify the clone.
XX Note: The sequence data for this patent did not form part of the printed
XX specification, but was obtained in CD-ROM format directly from EPO.

Sequence 665 BP; 147 A; 194 C; 190 G; 130 T; 4 other:

alignment_scores:
Quality: 775.50 Length: 169
Ratio: 4.847 Gaps: 2
Percent Similarity: 94.675 Percent Identity: 93.491

alignment_block:

US-09-762-491-6 x AAF44704

Align seg 1/1 to: AAF44704 from: 1 to: 665

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34 hrValPheAlaGlnAlaGlnAlaGlyTyrPheGlyAlaValLys 50
265 CAGGCTCCCGCGCAACATGAGAGTGGGCTACGATGCGCGTCAAG 314
51 IleValAsnSerLysAlaIleSerArgGluValIleAlaMetAlaSerLe 67
315 ATGTTAACTCGAAGCGCATATCCAGGGAGGTCAAGCGCATGCAAGCT 364
67 uAspArgGluPheValIleuArgGluGluValIleGluLysValAsnT 84
365 GAGTAAACGATTCCTGCTCCCTCAAGCGCTTATCGAAGAGTCAACT 414
84 rPheArgGlnAspProLysProAlaLeuValThrLysPheMetGluAsnGly 100
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101 SerLeuSerGlyLeuLeuGlnSerGlnCysProArgProTyrProLeuL 117
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167 InGly 168
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seq_name: /SIDSI/scgdata/hold-geneseq/geneeqn-emb1/NA2001A.DAT:AAF44704

seq_documentation_block:
ID AAF44704 standard: cDNA: 1073 BP.

AC AAF44704:

XX 27-MAR-2001 (first entry)

DE Novel protein kinase cDNA, SEQ ID NO: 85.

XX Human; mouse; protein kinase; antiarthritic; antisclerotic; osteopathic;
KW immunosuppressive; cardiac; renal; antiinflammatory; antiasthmatic;
KW dermatological; antidiabetic; antifertility; gene therapy; vaccine;
KW immune disorder; cardiovascular disease; neurodegenerative disease;
KW cancer; autoimmune disorder; stroke; inflammatory bowel disease;

KW Inflammatory pelvic disease; multiple sclerosis; psoriasis; ss.

XX Mus musculus.

OS WO200073469-A2.

XX 07-DEC-2000.

XX 26-MAR-2000; 2000MO-US14842.

XX 28-MAR-1999; 99US-0136503.

XX (SUGEN-) SUGEN INC.

XX Plozman GD, Martinez R, Whyte D, Sudersanam S;

XX MPI; 2001-032161/04.

XX P-PSDB; AAB65676.

PT Nucleic acids encoding kinase polypeptides, useful for diagnosing and
treating immune-related diseases and disorders, cardiovascular disease,
neurodegenerative diseases and/or cancers -

XX Disclosure: Fig 2; 310pp; English.

XX The present sequence encodes a novel protein kinase. The nucleic acids
and the protein kinases they encode may be used in the treatment and
diagnosis of diseases associated with inappropriate kinase expression
such as immune-related diseases and disorders, cardiovascular disease,
neurodegenerative diseases and/or cancers. The nucleic acids and
complementary sequences may also be used as DNA probes in diagnostic
assays. The kinase polypeptides may be used as antigens in diagnostic
of antibodies of kinase expression and activity. Anti-kinase antibodies
and kinase antagonists may also be used to down regulate kinase
expression and activity. Diseases related to kinase expression and
activity include rheumatoid arthritis, atherosclerosis, autoimmune
disorders, complications of organ transplantation, myocardial infarction,
CC immune disorders, cardiomyopathies, strokes, renal failure,
CC oxidative-stress related disorders, chronic inflammatory bowel disease,
CC chronic inflammatory pelvic disease, multiple sclerosis, asthma,
CC osteoarthritis, psoriasis, rhinitis, autoimmunity, diabetes, cancers and
CC reproductive disorders.

Sequence 1073 BP; 296 A; 289 C; 265 G; 223 T; 0 other:

alignment_scores:

Quality: 703.50 Length: 322
Ratio: 3.099 Gaps: 8
Percent Similarity: 70.497 Percent Identity: 50.311

alignment_block:

US-09-762-491-6 x AAF44704

Align seg 1/1 to: AAF44704 from: 1 to: 1073

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53 CCTGCTGTGGGAGTCTGCTGCTGCGAAGAGCTGATGTTGTAACAACA 102
226 rSerLeuValTyrGluAlaValCysAsnArgGlnAsnArgProSerLeu 242
103 CTTCACATAATCCGGAAACAGGTGTGACAGGACGAGCTCTCCACATG 152
243 AlaGluLeuProGlnAlaGlyProGluThrProGlyLeuGluLysLeuTyr 259
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326 LuMetArgGlyPheArgArgThrIleGluAlaGInHisSerArgAsnAsp 342
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51	IleValaAnSerLysAlaIleSerATrGluValLysAlaMetAlaSerLe	67
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67	wasPaspGluPhetAlaLeuArgLeuGluGlyValIleGluLysValAsnT	84
201	GGATPACGAAATTCGTGTGGCGCTTAAGAGGGGTATTCAGAAAGGTGAAC	250
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351	TTGCGCGCTCTCAAAAGATGGTGTGGGTGCTTTACCTGACGACACC	400
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1401 TATGCACACAGACAAAGCTTGCCCAATGAGGCTTGCCACTTCGGGCA 1450
484 yGgLYAaGgLYeUcGlnH1aPProProProValG1ySerGlnGlnGlyPro 500
1451 AGGGGAAGGGGCTTCGACGCCGCCCAACCAAGTAAGTTCGAAAGAGGCCCT 1500
501 LysAspProGln1a1aTPSerArgProGlnGlyTrrTYrAsnH15SerG1 517
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517 YLYs 518
1551 GAA 1554
seq_name: gb_pat:AR105328
seq_documentation_block: 1557 bp DNA linear PAT 14-FEB-2001
LOCUS AR105328
DEFINITION Sequence 2 from patent US 6096539.
ACCESSION AR105328
VERSION AR105328.1 GI:12818925
KEYWORDS
SOURCE
ORGANISM
UNCLASSIFIED.
1 (bases 1 to 1557)
AUTHORS Gomes,B,Charles, J, Kasof,G, M, and Prosser,J,Caroline.
TITLE Protein activator of apoptosis.
JOURNAL Patent: US 6096539-A 2 01-AUG-2000;
FEATURES
Location/Qualifiers
source
1..1557 /organism="unknown"
BASE COUNT 395 a 422 c 448 g 291 t 1 others
ORIGIN
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quality: 2744.00
length: 518

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Ratio: 5.328 Gaps: 0
Percent Similarity: 99.421 Percent Identity: 99.228

Alignment block:
US-09-762-491-6 x AR105328

Align beg 1/7 to: AR105328 from: 1 to: 1557

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DEFINITION Sequence 2 from Patent WO0077200.

ACCESSION AX067677

VERSION AX067677.1 GI:12329571

KEYWORDS

SOURCE human.

ORIGIN human.

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

REFERENCE 1 (bases 1 to 1557)
AUTHORS Gomez,B.C., Kasof,G.M. and Prosser,J.C.
TITLE Receptor interacting protein rip3
JOURNAL Patent: WO 0077200-A 2 21-Dec-2000;
Astrazeneca AB (SE)

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 DEFINITION Sequence 1 from patent US 6096539.
 ACCESSION AR105327
 VERSION AR105327.1 GI:12818924

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 1873)

AUTHORS Gomes,B,Charles., Kasof,G.M. and Prosser,J.Caroline.
 TITLE Protein activator of apoptosis
 JOURNAL Patent: US 6096539-A 1 01-AUG-2000;
 FEATURES Location/Qualifiers

source 1..1873

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ORIGIN

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VERSION AX067676.1 GI:12329570
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Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS Gomes B.C., Kasof G.M. and Prosser J.C.
TITLE Receptor interacting protein rlp3
JOURNAL Percent: W0077200-A 1 21-DEC-2000;
Astadeneca AB (SE)
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STS alignment scores:
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Ratio: 4.416 Gaps: 11
Percent similarity: 44.532 Percent identity: 44.269

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Align seg 1/1 to: AFL78953 from: 1 to: 1833

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seq_name: gb_pat:AX100029

seq_documentation_block: 1437 bp DNA linear PAT 02-APR-2001

LOCUS AX100029

DEFINITION Sequence 1 from Patent WO0119990.

ACCESSION AX100029

VERSION AX100029.1 GI:13539035

KEYWORDS

SOURCE

ORGANISM

Rattus sp.

Rattus sp.

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;

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REFERENCE      1 (bases 1 to 1437)
AUTHORS        Virca, C.D. and Bird, T.A.
TITLE          RLP-3-like death-associated kinase
JOURNAL        Patent: WO 011990-A 1 22-MAR-2001;
                IMMUNEX CORPORATION (US)
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DEFINITION Sequence 14 from patent US 5674734.
ACCESSION 168122
VERSION 168122.1 GI:2830244
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 2268)
AUTHORS Leder, P., Seed, B., Stanger, B. Z., Lee, T.-H. and Kim, E.
TITLE Cell death protein
JOURNAL Patent: US 5674734-A 14 OCT-1997;
FEATURES
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DEFINITION Mus musculus cell death protein (RIP) mRNA, complete cds.
ACCESSION U25995.1 GI:829618
VERSION U25995.1 GI:829618
KEYWORDS Fas; TNF receptor.
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ORGANISM Mus musculus
Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 2268)
Stanger,B.Z., Leder,P., Lee,T.H., Kim,E. and Seed,B.
RIP, a novel protein containing a death domain that interacts with
Fas/Apo-1 (CD95) in yeast and causes cell death
JOURNAL Cell 81 (4), 513-523 (1995)

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MEDLINE 95277838
REFERENCE 2 (bases 1 to 2268)
AUTHORS Stanger,B.Z.
JOURNAL Direct Submission
Submitted (01-MAY-1995) Ben Z. Stanger, Genetics, Harvard Medical
School, 200 Longwood Avenue, Boston, MA 02115, USA
FEATURES
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48 leuvalleuvalleuval.....serlysalalle 57
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seq_documentation_block: 3559 bp mRNA linear ROD 08-JAN-2002
LOCUS AF302127
DEFINITION Mus musculus PKC-regulated kinase prk mRNA, complete cds.
ACCESSION AF302127
VERSION AF302127.3 GI:18087895
KEYWORDS
SOURCE
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
Chen, L., Haider, K., Ponda, M., Carlepe, A., Rowitch, D. and Pilla, S.

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355 GIU.GIUPROSERSer.....ValPROLYSLeuCys..... 355
1097 GAAAGCCCGCCAGAGAGCTCAGAGCAAGTCTCTGATATCCAGACCTCCATC 1146
366 ..ProSerLeuThrLysArgSerArgAlaGlnGluGlnValIleProGln 381
1147 GTCCAGAGAGTGGCAAGAGGCTCTGGGGG.....TGTCCCTCAG 1184
382 AlaThrPheAlaGly.....ThrSerSe 389
1185 ...TGGACTCAGCCTTTCTCCAGAGATCGCTGACTGCTTTTGG 1231
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426 .....GlyAlaGlnArgGlnGlyMetAsnTrpSerC 436
1376 CTGCTGACCTGGCTGTGAGCGCCGACAGAGAGCTGTCAATGGCT 1425
436 ybaArgThrProGluProAsnProVal.....ThrGlyArgProLeu.Va 450
1426 GCTCTTACAAATCCAAACCCCACTGACACACAGAGAGGGCTCTCAC 1475
450 LAsnIleTyrAsnCysSer.....GlyValGlnIle 460
1476 CACTGATATGCTGTGGAGCGCAAGCGACGTGATTTGTGACTACTG 1525
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1526 CTACCCCGGAGACAGCTGCAATGCCAAGATGACACAGCTGACTGC 1575
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ACCESSION ARI45196
VERSION ARI45196.1 GI:15107063
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2016)
AUTHORS Balchwal,V.R., Huang,J., Hsu,H. and Goeddel,D.V.

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TITLE RIP: novel human protein involved in tumor necrosis factor signal
JOURNAL transduction
Patent: US 6211337-A 1 03-APR-2001;
FEATURES Location/Qualifiers
source 1..2016
BASE COUNT 629 a 446 c 514 g 427 t
ORIGIN

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Quality: 423.00 Length: 580
Ratio: 1.434 Gaps: 23
Percent Similarity: 50.862 Percent Identity: 25.862

alignment_block:
US-09-762-491-6 x ARI45196 ..
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33 yThrValPheArgAlaGlnHisArgLysTrpGly..... 44
87 GAAGCTGTCTGTCTGTTTCCACAGAACCCAGGACTCATGATGAA 136
45 ....TyrAspValAlaValLysIleValAsnSerLysAlaIleSerArg 59
137 CAGTGTACAGGGGCCCACTGATGTAGCACACAGAGCCCTCTTGAG 186
60 GluValLysAlaMetAlaSerLeuAspAsnGluPheValLeuArgLeuG1 76
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76 uGlyValIleGluLysValAsnTrpAspGlnAsnProLysProAlaLeu 93
237 GGCGCTCATC.....ATAGAGAGGAGGATCTCCCTGG 271
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272 TGAATGATACATGAGAGAGGCACTGATGCAGTGTGTAAGCCGAG 321
110 CysProLysProTrpProLeuLeuCysArgLeuLeuLysGluValVal 126
322 ATGAGTACTCCGCTTCTGTAAGAGATATATTTGGAAATCATATCA 371
126 uGlyPheThrTyrLeuHisAspGlnAsnProValLeuLeuHisArgAspL 143
372 AGCAATGTGCTACTTACATGAAAGGC.....GTGATACCAAGAGAC 415
143 eLysPProSerAsnValLeuProAsnProGluLeuHisValLysLeuAla 159
416 TCAACCTGAAATATATCTTGTGTATATGATCTCCACATTAAAGTCCA 465
160 AspPheGlyLeuSerThrPheGlnGlyLysSerGln..... 171
466 GACCTGGGCTTCCCTCTTAAGATGTGACCAAACTGAATATGAAGA 515
172 .....SerGlyThrGlySerGlyLysGlnProGlyG 181
516 GCACAATGAGCTGAGGAGAGTGCAGCGCACGCTAAG...AAGATGGCG 562
181 yThrLeuGlyTyrLeuAlaProGluLeuPheValAsnValAsnArgLys 197
563 GCACCTTACTACATGCGCCGAGCACCTCAATAGATCAACAGCAAG 612
198 AlaSerThrAlaSerAspValTyrSerPheGlyTyrIleuMetTrpAla 214
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231  lualavalCysaenArgIn.....AsnArg 239
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824  GCGCGACATTT.....CTGCGCATTTGAAGAAAAATTAGGCGCT 861
289  .....MetValGluAsnAsnMetAlaAlaValSerThrVa 301
862  TTTTATTATGATCATTAAGAGAAAGCTGAGAGAGAGAGCTGAAGATT 911
301  lLysAspPheLeuSerGlnLeuLysSerSerAsnArgPhe..... 315
912  AAGAGAAAGATATTCAACGCAAAATGCACTGTGAAGAAATGCAGTCTC 961
316  .....SerLeuProGluSer..... 320
962  TTCAACTTATGTTGTGGCAGTACCTTCAAGCCGCTCAAAATTCACGCCA 1011
321  .....GlyGlnGlyGlyTh 325
1012  GAACAGCTGTGCTGCTGACGACAGTCCAGGAGCTGGATGGCTCTG 1061
325  rGluMetAspGlyPheArgArgThrIleGluAsnGlnHisSerArgAsnA 342
1062  GGAGAGCTCTGCTGTTCCTCTCCCTGCGACGCCACAGAAAGAGATG 1111
342  sP.....ValMet 344
1112  AGCCAGCTGTGCAAGATGAACCTCAAGAGAGAAAGCAATACCATCTTAT 1161
344  tValSerGluThrLeuAsnLysLeuAsnLeu..... 355
1162  GGCAGCGCATGGACAGCAGCAAGAAACAGCCCGACAGAGAAATGTGCC 1211
356  .....GluProProSerSerVal 361
1212  TTACAAACAGAGAGAGAAAGCAGACGAGCTCTCCATGACCCCTTTTG 1261
362  ProLysLysCysProSerLeuThrLysArgSerArgAlaGlnGluG1 378
1262  CACAGCAAA.....GACCTTAGAGAAATTTTCAGAAATACAGAGGAAA 1305
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1356  CTCAGGGCTACACCACTCAAGTACTGATACAGAAACAATGATTAAT 1405
386  .....GlyThrSerSerAspSerMetAlaGlnProProGlnTh 398
1406  ATAGCTACATGCTTTGGACAAAGACACTGATCCAGCAACAGCAGCT 1455
398  rProGluThrSerThrPheArgAsnGlnMetProSerProThrSerThg 415
1456  CCCGAGCTTGTGTACAG.....CCAATTCCAAGTC 1486
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1487  ATATGCTATGCTGATTAATATCCAGTGCCTGAGACCACTATCTAGCA 1536
428  GluArgGlnGlyMetAsnTrpSerCysArgThrProGluProAsnProVa 444
1537  AATACACCCACCATGCCATTCACCTCTGCGCCACCMACAGATGAATCTAT 1586
444  lThrGlyArgProLeuValAsnIleTyrAsnCysSerGlyValGlnValG 461
1587  AAAA.....TATACATATACAAATAGTACTGCGATTCAGATTG 1624
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Date: Aug 13, 2002 10:43 PM

About: Results were produced by the GenCore software, version 4.5.
Copyright (c) 1993-2000 Compugen Ltd.

Command line parameters:

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-MNMATCH-0.100 -LOOPT-0.000 -LOOEXT-0.000 -GAPOP-6.000
-GAPEXT-0.050 -YGAPOP-10.000 -YGAEXT-0.500 -FGAPOP-6.000
-DELXT-7.000 -START-1 -MATRIX-biosum62 -TRANS-human40.cdl
-LIST-45 -DOALIGN-200 -THR SCORE-pct -THR MAX-100 -THR MIN-0
-ALIGN-15 -MODE-LOCAL -OUTFMT-pfs -NORM-est -HEAPSIZE-300
-MNM-0 -MAXLEN-200000000 -USP-US09/62491_153857_4927
-NCPI-6 -ICPU-3 -LONGLOG -DEV-TIMEOUT-120 -MARK-TIMEOUT-30
-NO_XLAPX -WAIT -THREADS-1

Search information block:

Query: US-09-762-491-6
Query Length: 519
Database: EST: *
Database sequences: 13736207
Database Length: 1841457050
Search time (sec): 1589.130000

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gb_est2:BF116301	927.50	1122.92	1.2e-53	643	BF001916 79350C01 X1 NCI_CGAP_C
gb_est2:BF116301	804.50	978.33	3.0e-45	758	AL601137 DK2P31300939_F1 313
gb_est2:BF116301	779.00	949.28	1.6e-43	906	BI905455 603167947F1 NCI_CGAP_C
gb_est2:BF116301	760.00	929.44	1.3e-42	616	BI833763 603088473F1 NIH_MGC_12
gb_est2:BF116301	698.50	848.28	5.3e-38	821	AA227673 zt55d09_X1 Soares_Nhh
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gb_est2:BF116301	668.00	817.44	2.8e-36	432	BI413255 602986395F1 NCI_CGAP_C
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DEFINITION	Mus musculus 10 days embryo whole body cDNA, RIKEN full-length enriched library, clone:2610528K09; similar to RECEPTOR INTERACTING PROTEIN 3, full insert sequence.			
ACCESSION	AK012177	GI:12848761		
VERSION	AK012177.1			
KEYWORDS	HTC; CAP trapper.			
SOURCE	Mus musculus (strain:G57BL/6J) 10 days embryo cDNA to mRNA, clone:11b:RIKEN full-length enriched mouse cDNA library			
ORGANISM	Mus musculus			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.			
AUTHORS	1 (altes)			
TITLE	Carninci, P. and Hayashizaki, Y.			
JOURNAL	High-efficiency full-length cDNA cloning			
PUBMED	Meth. Enzymol. 303, 19-44 (1999)			
REFERENCE	99279253			
AUTHORS	2 (altes)			
TITLE	Carninci, P., Shibata, Y., Hayatsu, N., Suganara, Y., Shibata, K., Itoh, H., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.			
JOURNAL	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes			
PUBMED	Genome Res. 10 (10), 1617-1630 (2000)			
REFERENCE	3 (altes)			
TITLE	Shibata, K., Itoh, H., Aizawa, K., Nagao, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kikunishi, T., Tashiro, H., Itoh, M., Suni, N., Ishii, Y., Nakamura, S., Hazama, M., Nishino, T., Harada, K., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujikawa, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watabiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuyama, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.			
JOURNAL	RIKEN Integrated sequence analysis (RISA) system -184-format			
PUBMED	sequencing pipeline with 384 multipipillary sequencer			
REFERENCE	Genome Res. 10 (11), 1757-1771 (2000)			
AUTHORS	4 (altes)			
TITLE	The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.			
JOURNAL	Functional annotation of a full-length mouse cDNA collection			
PUBMED	Nature 409, 685-690 (2001)			
REFERENCE	5 (Pages 1 to 1855)			
AUTHORS	Aachari, J., Aizawa, K., Akahira, S., Akimura, T., Aono, H., Arai, A., Arakawa, T., Baldarelli, R., Bono, H., Brownstein, M., Bult, C., Carninci, P., Fukuda, S., Fukunishi, Y., Furuno, M., Hanegeti, T., Hara, A., Hayatsu, N., Hill, D., Hiramoto, K., Hirotsu, T., Hori, F., Hume, D., Imatani, K., Ishii, Y., Itoh, M., Izawa, M., Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Konno, H., Kouda, M., Koyu, S., Numaaki, R., Ohno, M., Okazaki, Y., Okido, T., Owa, C., Quackenbush, J., Saito, H., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Schirml, L., Shibata, K., Shibata, Y., Shingawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takehashi, F., Tanaka, T., Teijima, Y., Toyu, T., Yamamura, T., Yamashita, I., Yanagisaki, Y., Yoshida, K., Yoshino, M., Muramatsu, M. and Hayashizaki, Y.			
TITLE	Direct Submission			
JOURNAL	Submitted (10-JUL-2000) Yoshinori Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC),			


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VERSION    BI770357.1 GI:15761935
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SOURCE     human.
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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REFERENCE  1 (bases 1 to 929)
AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL    Unpublished (1999)
COMMENT    Contact: Robert Strausberg, Ph.D.
            Email: cgabs-remail.nih.gov
            Tissue Procurement: Life Technologies, Inc.
            cDNA Library Preparation: Life Technologies, Inc.
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
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            High quality sequence stop: 870.
            Location/Qualifiers
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            Site.1: NotI; Site.2: EcoRV (destroyed); RNA source
            anonymous pool of 24 week female lung, 16 week female
            spleen, and 20-22 week male spleens. Library is oligo-dT
            primed and directionally cloned (EcoRV site is destroyed
            upon cloning). Average insert size 1.4 kb, insert size
            range 1-3 kb. Library is normalized and enriched for
            full-length clones and was constructed by C. Gruber
            (Invitrogen). Research Genetics tracking code 026. Note:
            this is a NIH MGC library."
BASE COUNT  203 a 271 c 276 g 179 t
ORIGIN

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219 CATCCAGGAACTGAGCAACGAGACCTCTCGCAAAAGCGGCTTGGCA 268
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419 GGGACCAAGATCCCAAGCCGGCTCTGGTCACTAAATTCATGGAGAACGGC 468
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101 SerLeuSerGlyLeuLeuGlnSerGlnCysProArgProTTPProLeuLe 117
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
469 TCCCTGTGCGGGCTGCTGCGAGTCCAGTCCCTCGCGCTTGGCGCTTCT 518
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
117 uCysArgLeuLeuLysGlnValValI11eGlnLysMetPheTyrLeuHisAspG 134
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
519 TTGCGCGCTGCTGAAGAAAGATGGTGGTGGGATGTTTACCTGCACAGAC 566
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
134 lAsnProValLeuLeuHisArgAspLeuLysProSerAsnValLeuPro 150
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
569 AACACCCGCTCTCTCTGACCGGACCTCAACGATCCAAAGCTCTGCTG 618
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
151 AAPPProGluLeuHisValLysAlaAlaAspPheGlyLeuSerThrPheG1 167
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
619 GACCGAGAGCTGCACGTCAAGCTGGCAGATTTTTCGCTGTCACAACTTCA 668
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
167 nGlyLysSerGlnSerGlyThrGlySerGlyGluProGlyGlyThrLeuG 184
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
669 GGGAGGCTCAGATCAGGAGGAGGTCGGGAGCCAGGGGACCCCTGG 718
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
184 lTyrTLeuAlaProGluLeuPheValAsnValAsnArgLysAlaSerTh 200
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
719 GCTACTTTGGGCCCGAAGATGTTGTACCGTAACCGGAGGCGCTCCAC 766
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
200 rAlaSerAspValTyrSerPheGlyI11eLeuMetTrrPalValLeuAlaG 217
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
769 ACCAGTACCTCTACACCTTCGGCATTCATATGTCGGCAGCTTGGCTT 818
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
217 lYArgGlu...ValGluLeuProThrGluProSerLeuValTyrGluAla 232
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
819 GGAAGAGAAAGTGCAGTTCACCAACGAACTTCATCTGTGTAGCAAGCA 868
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
233 'ValCysAsnArgGlnAsnArgProSerLeuAlaGluLeuProGlnAlaG 249
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
869 ACTGTGCACAGCGCAAGAACCGGCTTCATTGTGTGAGCTGGCCCAACCGCG 918
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249 lY 249
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919 GC 920

seq_name: gb_est2:BI819557

seq_documentation_block:
LOCUS   BI819557          1026 bp    mRNA    linear    EST 04-OCT-2001
DEFINITION  603036778F1 NIH_MGC_115 Homo sapiens cDNA clone IMAGE:5177994 5',
      mRNA sequence.
ACCESSION  . BI819557
VERSION    BI819557.1 GI:15931107
KEYWORDS   EST.
SOURCE     human.
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

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REFERENCE 1 (bases 1 to 1026)
 AUTHORS NIH-MGC <http://mgc.ncl.nih.gov/>
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgabs-remail.nih.gov
 Tissue Procurement: Life Technologies, Inc.
 cDNA Library Preparation: Life Technologies, Inc.
 DNA Sequencing by: Incyte Genomics, Inc.
 clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
 Plate: L14M1143 row: k column: 19
 High quality sequence stop: 860.

FEATURES
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 Location/Qualifiers
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:517994"
 /clone_lib="NIH-MGC_115"
 /lab_host="DH10B"
 /note="Organ: pooled brain, lung, testis; Vector: pCMV-Sport6; Site: 1: NotI; Site: 2: EcoRV (destroyed); RNA source anonymous pool of 6 male brains, age 23-27; 1 male lung, age 27; and 1 male testis, age 69. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size is 1.8 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 021. Note: this is a NIH-MGC Library."

BASE COUNT 230 a 298 c 298 g 198 t 2 others
 ORIGIN

alignment_scores:
 Quality: 1171.00 Length: 296
 Ratio: 4.369 Gaps: 13
 Percent Similarity: 90.541 Percent Identity: 86.149

alignment_block:
 US-09-762-491-6 x B1819557 ..

Align seg 1/1 to: B1819557 from: 1 to: 1026

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17 TTTGGTCTGCTCAAGTATAGGCCCGCGGTGCCCCCGCTTGGTCTC 34
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198 CATCGAGCAAGTATAGGCCCGCGGTGCCCCCGCTTGGTCTC 247
|||||
34 hValAlaPheArgAlaGlnHisArgLysTrpGlyTyrAspValAlaValLys 50
|||||
248 CAGTGTTCCTGCGGCGCACTATAGGAGTGTACGATGCGCGTTCAG 297
|||||
51 TLeValAsnSerLysAlaIleSerArgLysValLysAlaMetAlaSerLe 67
|||||
298 ATCGTAACTTCGACGCGATATCCGAGGTTCAGGCGCATGCCAAGTCT 347
|||||
67 uAspArgGlnPheValIleuArgLeuGlyValIleGlyLysValAsnTr 84
|||||
348 GGTATACGAATTCGTGCTGCGCTAGAGGGGTATCGAGAGGTGAACT 397
|||||
84 rPheAlaPheProLysProAlaLeuValIleLysPheMetGluAsnGly 100
|||||
398 GGGACCAAGATCCCAAGCGGCTGTGGTAAATTCATAGGAGAAAGGCG 447
|||||
101 SetLeuSerGlyLeuLeuGlnSerGlnCysProArgProTrpProLeu 117
|||||
448 TCCTTGTCCGGGCTGCTCGACATCCAGTCCCGCTGCGCGCTCTCT 497

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117 uCyArgLeuLeuLysGluValValLeuGlyMetPheTyrLeuHisAspG 134
|||||
498 TTGCGGCTGCTGAAAGAGGTGCTTGGGATGTTTACTCTCAGCACC 547
|||||
134 InAsnProValIleuLeuHisArgAspLeuLysProSerAsnValLeuPro 150
|||||
548 AGAACCCGGTGTCTTCGACCGGAGCTCAAGCCATCCAAAGTCCCTGG 597
|||||
151 AspProGlnLeuHisValLysLeuValAspPheGlyLeuSerThrPheG 167
|||||
598 GACCCAGAGCTGCACGCTCAAGCTGCGAGATTTTGGCTTCCACATTTC 647
|||||
167 nGlyGlySerLeuSerGlyThrGlySerGlyGluProGlyGlyThrLeu 183
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648 GGGAGGCTCAGTCAAGGAGCAGGGTCCGGGAGCCAGGGGACCCCT... 694
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184 GlyTyrLeuAlaProGlnLeuPheValAsnValAsnArgLysAlaSerTh 200
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695 GGGCTACTCGCCCGACAGACTGTTGTAACTTAACCGAAGGTCCTCCAC 744
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200 rAlaSerAspValTyrSerPheGlyTyrLeuMetTrpAlaValAlaVal 216
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745 AGCCAGTACGCTACACGCTCGGATTCCTTAATGCGGACGCTTCTCT 794
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217 GlyArgGluValGluLeuProThrGluProSerLeuValTyrGlnA 232
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795 GGAAGAGAACGTTGAGTGCACCAACCGAACCACTCTGTTAGGAAG 844
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233 ValAlaCysAsnArgGlnAsnArgPro...SerLeuAlaGluLeuProG 247
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845 CAGGTGTCACAGGAGCAAGACCGGCTTCAATGATGCTGCTGCCCA 894
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247 nAlaGlyProGlnLeuThrProGlyLeuGlnGlyLeuLysGlnLeuMetG 264
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895 AGCCGGCTGAGTTCCTCGGATTAAGGCTCGCAAGGCTAATTCCTCC 944
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264 euCys.TyrSerSerGluProLysAspArgProSerPheGlnGlyCysL 280
|||||
945 TCTTGGGAGACGACGATGACCCAG...AAAAGCTCTCTCAGATGTCGA 991
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992 CC...AAACGTAGTAAGTC 1008
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seq_documentation_block:
LOCUS B1838468 897 bp mRNA linear EST 04-OCT-2001
DEFINITION 603083449P1 NIH-MGC_120 Homo sapiens cDNA clone IMAGE:522316 5',
mRNA sequence.
ACCESSION B1838468
VERSION B1838468.1 GI:15950018
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 897)
AUTHORS NIH-MGC http://mgc.ncl.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: L14M1159 row: b column: 13
High quality sequence stop: 888.

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FEATURES
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Location/Qualifiers
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/clone="IMAGE:5222316"
/clone_lib="NIH_MGC_120"
/lab_host="DH10B"
/note="Organ: pooled pancreas and spleen; Vector:
pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA
source anonymous pool of spleen and pancreas from 28 yo
male. Library is oligo-dT primed and directionally cloned
(EcoRV site is destroyed upon cloning). Average insert
size 1.5 kb, insert size range 1-2.5 kb. Library is
normalized and enriched for full-length clones and was
constructed by C. Gruber (Invitrogen). Research Genetics
tracking code 023. Note: this is a NIH_MGC library."

BASE COUNT 193 a 263 c 266 g 175 t

ORIGIN

alignment_scores:
Quality: 1159.00 Length: 250
Ratio: 4.770 Gaps: 1
Percent Similarity: 97.200 Percent Identity: 96.400

alignment_block:
US-09-762-491-6 x B1839468 ..

Align seg 1/1 to: B1839468 from: 1 to: 897

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17 TTTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 34
|||||
193 CATCGAGCAACTGGAACAGAGAGCTGCTGGCAAGAGCGGTGGCA 242
|||||
34 hTValPheArgAlaGlnHisArgValTrpGlyTyrAspValAlaValys 50
|||||
243 CAGGTGTCGGGGCCAGCAATGAGAGAGAGAGAGAGAGAGAGAGAG 292
|||||
51 TLeValAsnSerLybAlaIleSerArgGluValLybAlaMetAlaSerLe 67
|||||
293 ATCCCTAACTCGAAGCGATATCCAGGAGTCAAGGCCATGCGCAACTC 342
|||||
67 uAPAsnGluPheValLeuArgLeuGluGlyValTLeGluValAlaSer 84
|||||
343 GGAATACGAATTCGTCTGCGCTAGAGGGCTTATCGAGAGGTGAAC 392
|||||
84 rPAspGlnAspProLySProAlaLeuValTThrLybPheMetGluAsnGly 100
|||||
393 GGGACCAAGATCCCAAGCGCGCTGTGTACTAAATTCATGAGAACGGC 442
|||||
101 SerLeuSerGlyLeuLeuGlnSorGlnCysProATGProTTPProLeuLe 117
|||||
443 TCTTGTGCGCGCTGCTGCGAGTCCAGTCCCTCGCGCTGCGCTGCT 492
|||||
117 uCyAArgLeuLeuLybGluValValLeuGlyMetPheTyrLeuHisAspG 134
|||||
493 TTGGCGGCTGCTGAAAGAGTGTGTTGGATGTTTAACTGACACAGCC 542
|||||
134 LAsnAspValLeuLeuHisArgAspLeuLySProSerAsnValLeuPro 150
|||||
543 AGAACCCGGTGTCTGACACCGGACCTCAACCCATCCAACTCTCTCTG 592
|||||
151 AsPProGluLeuHisValLybAlaAspPheGlyLeuSerThrPheGln 167
|||||
593 GACCCAGAGCTGCACGTCAAGCTGCAGATTTTGGCGTCTCAACATTTCA 642
|||||
167 nGlyGlySerGlnSerGlyThrGlySerGlyValProGlyValThrLeu 183
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643 GGGAGGCTCAACAGTCAAGGAGAGAGGTCGGGGAGCCAGGGGCGCTGT 692
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184 GlyTyrLeuAlaProGluLeuPheValAsnValAlaAsnArgLybAlaSerTh 200
|||||
693 GGCTACTGTGGCCAGAACTGTTGTAAAGTAAACCGAAGGCCCTCCAC 742
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200 rAlaSerAspValTyrSerPheGlyTyrLeuMetTrpAlaValLeuAlaG 217
1 |||||||
743 AGC.AGTACGCTTACAGCTTCGGATCCTAATGTGGCAGTCTGCTG 791
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217 LyAGluValAlaGluLeuProThrGluProSerLeuValTyrGluAlaVal 233
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792 GAAGGAAAGTTGAGTTCGCAAC.GAACCATCATCGGTGTCCAAAGCAGTG 840
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234 CyAsnArgGlnAsnArgProSerLeuAlaGluLeuProGlnAlaGly 249
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841 TCCACACGACGCAAGCCGCT.TCCTTGGCTGAGCTGCCCAAGCCGGCG 887

seq_name: gb_cst2:B1823411

seq_documentation_block:
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DEFINITION 603041149F1 NIH_MGC_115 Homo sapiens CDNA clone IMAGE:5181972 5',
mRNA sequence.
ACCESSION B1823411
VERSION B1823411.1 GI:15934961
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 922)
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgrahs-remail.nih.gov
Tissue procurement: Life Technologies, Inc.
CDNA library preparation: Life Technologies, Inc.
CDNA library arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLNL1454 row: a column: 13
High quality sequence start: 2
High quality sequence stop: 785.

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/clone_lib="NIH_MGC_115"
/lab_host="DH10B"
/note="Organ: pooled brain, lung, testis; Vector:
pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA
source anonymous pool of 6 male brains, age range 23-27; 1
male lung, age 27; and 1 male testis, age 69. Library is
oligo-dT primed and directionally cloned (EcoRV site is
destroyed upon cloning). Average insert size 1.8 kb,
insert size range 1-3 kb. Library is normalized and
enriched for full-length clones and was constructed by C.
Gruber (Invitrogen). Research Genetics tracking code
021. Note: this is a NIH_MGC library."

BASE COUNT 206 a 269 c 270 g 177 t

ORIGIN

alignment_scores:
Quality: 1099.50 Length: 252
Ratio: 4.659 Gaps: 8
Percent Similarity: 93.651 Percent Identity: 92.063

alignment_block:

us-09-762-491-6 x B1823411 ..

Align seg 1/1 to: B1823411 from: 1 to: 922

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|||||
223 CATCGAGGAAGCTGGAGAACCAAGACCTGCTCGCCAAAGCCGCTCGCA 272
34 hValAlaPheArgAlaGlnHisArgGlyTTPGlyTTPAspValAlaValLys 50
|||||
273 CAGTCTCCGGCGGCACATAGCAAGTGGCTGATGATGGCGCTCAAG 322
51 lIleValAsnSerLysAlaIleSerArgLysValLysAlaMetAlaSerLe 67
|||||
323 ATCGTAAACTCGAAGCGCATATCCAGAGGTCAGAGCCATGCCAAGTCT 372
67 uAspArgLysPheValLeuArgLeuGluGlyValIleGluLysValAsnT 84
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373 GGATTAACGAATTCGTCTGCTCGCTTGAAGGGTTATTCAGAAAGTGAACT 422
84 rPAspGlnAspProLysProAlaLeuValIThrLysPheMetGluAsnGly 100
|||||
423 GCGACCAAGATCCAGACCGCCTCTGCTGAATTCATGAGAACGGCC 472
101 SerLeuSerGlyLeuLeuGlnSerGlnCysProArgProTrpProLeuLe 117
|||||
473 TCCTTGTGCGGGGTGCTGTCAGTCCAGTCCCTGGCCCTGGCCGCTCC 522
117 uCysArgLeuLeuLysGlnValValLeuGlyMetPheLysLeuHisArg 134
|||||
523 TTGCGCCCTGCTGAAGAAAGTGTCTGGGATGTTTACCTGACAGACC 572
134 lAsnArgValLeuLeuHisArgAspLeuLysProSerAsnValLeuPro 150
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151 AspProGluLeuHisValLysLeuAlaAspPheGlyLeuSerThrPheGly 167
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167 nGlyGlySerGlnSerGlyThrGlySer.GlyGluProGlyGlyThrLeu 183
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673 GGGAGGCTCACAGTCAGGACAGGCTCCGGGAGCCAGGGGCGACCTG 722
184 GlyTyrLeuAlaProGlyLeuPheValAsnVal.AsnArg.LysAlaSer 199
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723 GCGTACTTGTGCCCAAGACTGCTGTAAAGTAAACGGAAAGGCTGCTC 772
200 ThrAlaSerAspVal.TyrSerPhe.GlyTyrLeuMet.TTpalAlaValLe 215
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773 ACAGCCAGTACGATCTACAGTCTCCGGGATCTTAATGTTGGCAGTGGCT 822
215 uAlaGlyArgGlu...ValGluLeuProThrGluProSerLeuValTyrG 231
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823 TCGTGGAAAGAAACAGTTGAGTGGCAACCGAAGCATCACTGCTAGAG 872
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seg_name: gb_est1:AW959157

seg_documentation_block:

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LOCUS      AW959157                630 bp      mRNA      linear      EST 01-JUN-2000
DEFINITION EST371227 MAGE resequences, MAGF Homo sapiens cDNA, mRNA sequence.
ACCESSION  AW959157
VERSION    AW959157.1 GI:8148841
KEYWORDS   EST.
SOURCE      human.

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ORGANISM

Homo sapiens

REFERENCE 1 (bases 1 to 630)
Mammalia: Eutheria: Primates: Catarrhini: Hominoidea: Homo.

AUTHORS

Hegde, P., Qi, R., Abernathy, R., Dharap, S., Gaspard, R., Gay, C., Holt, I. E., Saeed, A. I., Sharov, V., Lee, N. H., Yeatman, T. J. and Quackenbush, J.

TITLE

Assessment of gene expression patterns in a model of colon tumor metastasis using a 19,200 element cDNA microarray

JOURNAL

Unpublished (2000)
Contract: John Quackenbush

COMMENT

The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 3528
Fax: 301 838 0208
Email: johnq@tigr.org
Plate: 130

FEATURES

Seq primer: Reverse.

Location/Qualifiers
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="MAGE resequences, MAGF"
/note="Vector: pBluescriptSM"

BASE COUNT

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ORIGIN

Alignment_scores:

Quality: 1070.00 Length: 210
Ratio: 5.169 Gaps: 1
Percent Similarity: 98.571 Percent Identity: 96.667

Alignment_block:

us-09-762-491-6 x AW959157 ..

Align seg 1/1 to: AW959157 from: 1 to: 630

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|||||
52 GGTAAAGGATTTCTCTCTCAGCTCAGAGAGCAATAGAGATTTTCTA 101
317 lProGluSerGlyGlnGlyThrGluMetAspGlyPheArgArgThr 333
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102 TCCAGAGTCAGGCCCAAGAGGACGACAGAAATGATGCTTTAGAGAAC 151
334 lLeGluAsnGlnHisSerArgAsnAspValMetValSerGluThrLeuAs 350
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152 ATAGAAACCAAGCACTCTGCTATATATATGATGCTTCTAGAGCTA 201
350 nLysLeuAsnLeuGluLysProProSerSerValProLysLysCysProS 367
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202 CAACCTAATCTAGACAGACCTCCAGCTGCTTCCCTAAATAATGCCGA 251
367 eLysuThrLysArgSerArgAlaGlnGluGluGlnValProGlnAlaTrp 383
|||||
252 GCGTTACCAAGAGACGACGACAGCAAGAGAGAGAGTTCACAAAGCTG 301
384 ThrAlaGlyThrSerSerAspSerMetAlaGlnProProGlnThrProG 400
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302 ACAGCAGGACATCTTCAGATTCAGATGCGCCACCTCCACAGACTCCAGA 351
400 uThrSerThrPheArgAsnGlnMetProSerProThrSerThrGlyThrP 417
|||||
352 GACCTCAACTTTCAGAAACAGATGCCAGCCCTACCTCACTGCAACAC 401
417 rAspArgProGlyProArgGlyAsnGlnGlyAlaGluArgGlnGlyMetAsn 433
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402 CAATCTCTGAGCCCGAGGAATTCAGAGGCGCTGACAGACAGACATGAAC 451

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434 TtpSerCysArgThrProGluProAnProValThrGlyArgProLeuVa 450
 432 TGGTCCTGACAGACCGCGGAGCCAAATCCAGTACAGGCGACCGCTCT 501
 450 TAsnIleGlyAsnGlySerGlyValGlnValGlyAspAsnAntyLeuT 467
 502 TACATATACAACTGCTCTGGGTGCMAAGTTGAGACAACTACTGA 551
 467 hTMeGlnGlnThrAlaLeuProThrTTPGlyLeuAlaPro.SergI 483
 532 CTATCAACAGACACTGCTTGGCCAAAGGCGCTTGCACCTTTCGGG 601
 483 yLysGlyArgGlyLeuGlnHisProPro 492
 602 CCAAGGAGAGGGGTTCGACACCCCCCC 629

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 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 1 (bases 1 to 643)
 NCI_CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 Unpublished (1997)
 JOURNAL Contact: Robert Strausberg, Ph.D.
 COMMENT Email: cgep@bcrfemail.nih.gov
 Tissue Procurement: Ilian Kirsch, M.D., Michael R. Emmert-Buck, M.D.,
 Ph.D.
 CDNA Library Preparation: M. Bento Soares, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/BLNT, send email to:
 info@image.llnl.gov
 Seq primer: -40bp from GIBCO
 High quality sequence stop: 166.

FEATURES
 source
 1..643
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:3314226"
 /clone_11b="NCI_CGAP_Col6"
 /tissue_type="colon tumor, RER"
 /lab_host="DH10B"
 /note="Organ: colon; Vector: pUT3D-Pac (Pharmacia) with a
 modified polylinker; Site: 1. Not 1; Site: 2. Eco RI.
 Plasmid DNA from the normalized library NCI_CGAP_Col6 was
 prepared, and 89 circles were made in vitro. Following HAP
 purification, this DNA was used as tracer in a subtractive
 hybridization reaction. The driver was PCR-amplified cDNAs
 from a pool of 5,000 clones made from the same library
 (clonoids 1057416-1061255, and 1144584-1145311).
 Subtraction by Bento Soares and M. Fatima Bonaldo."

BASE COUNT 129 a 166 c 162 g 186 t
 ORIGIN

alignment_scores:
 Quality: 927.50 Length: 234
 Ratio: 4.831 Gaps: 2
 Percent Similarity: 82.051 Percent Identity: 76.068

alignment_block:
 US-09-762-491-6 x BF001916/rev ..
 Align seg 1/1 to reverse of: BF001916 from: 1 to: 643

286 ValPIeGlnMetValGluAsnAsnMetAsnAlaValSerThrVally 302
 643 GTCCTCAAGATGGTGCACTAATATCAATCAATGCGGCTTACACGGTAA 594
 302 sApPheLeuSerGlnLeuLysSerSerAsnArgArgPheSerIleProG 319
 593 GGATTTCTCTGATATCGTTACAGACAGCAATATGAGATGTATATCCAG 544
 319 LysSerGlyGlnGlyThrGlnMetAspGlyPheArgGlyThrIleu 335
 543 ACAGATCTAGAGAGGACACATATGATGAGTGGCTCTAGGAGATCTT 494
 336 AaGlnHisSerArgAsnAspValMetValSerGluTrpLeuAsnLysLe 352
 493 AACCAACACTCTCGTAATGATGTCATGTTCTGAGTGAACATCTG 444
 352 uAsnLeuGluGluProProSerSerValProLysLysCysProSerLeuT 369
 443 ACATGTAGAGAGCCCTCCAGATTGTGTCCTAATATATGCCCGACCTTA 394
 369 hTlyArgSerArgAlaGlnGluGlnValProGlnAlaTrpThrAla 385
 393 CCAGAGAGACAGGACACAAAGAGCAGGTTCCACACACTCGACACCA 344
 386 GlnTrpSerSerAspSerMetAlaGlnProProGlnThrProGlnThrSe 402
 343 GGCACATCTTCAGATATGATGCGCCAACTCCCACTCCCACTCA..... 302
 402 rThrPheArgAsnGlnMetProSerProThrSerThrGlyThrProSerP 419
 302 302
 419 rodLyProArgGlyAsnGlnGlyAlaGluArg.GlnGlyMetAsnTrpSe 435
 301 GAGCAAGGCACTGCACTGCTG 281
 435 rCysArgThrProGluProAnProValThrGlyArgProLeuValAsnI 452
 280 CTGCAAGAGCCCGGAGCCAAATCCAGTAACAGGCGACCGCTGTACCA 231
 452 tEtyrAsnGlySerGlyValGlnValGlyAspAsnAntyLeuThrMet 468
 230 TATACACTGCTCTGGGTGCMAAGTTGAGACAACTACTTGAATG 181
 469 GlnGlnThrThrAlaLeuProThrTTPGlyLeuAlaProSerGlyLysG 485
 180 CAACAGACAACTGCTTGCACATGCGCTTGCACCTCGCGCCACAGCG 131
 485 yArgGlyLeuGlnHisProProProValGlySerGlnGluGlyProLysA 502
 130 GAGGGGCTTGCAGACACCCCCACCACTAGTTTCGCAAGAGCCCTTAAG 81
 502 sProGlnAlaTrpSerArgProGlnGlyTrpTyrAsnHisSerGlyLys 518
 80 ATCTGAAGCTTGAGAGGACAGGAGGTTGGTATATCATATAGCGGAAA 31

seq_name: gb_est1:AL601137
 seq_documentation_block: 758 bp mRNA linear EST 14-AUG-2001
 LOCUS AL601137 DKFZ31300939.t1 313 (synonym: hlc2) Homo sapiens CDNA clone
 DEFINITION DKFZ31300939 5', mRNA sequence.
 ACCESSION AL601137
 VERSION AL601137.1 GI:15164643
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE 1 (bases 1 to 758)
 AUTHORS Duesterhoeft, A., Lauber, J., Meves, H.W., Casenhuber, J. and Wiemann, S.
 TITLE EST (Duesterhoeft, et al.)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Duesterhoeft A
 MIRS

Am Klopferstr. 18a D-82152 Martinsried, Germany
 This is the 5' sequence of the clone insert
 Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ), Email: s.wiemann@dkfz-heidelberg.de;
 sequenced by Oligen (Hilden/Germany) within the cDNA sequencing consortium of the German Genome Project.
 No 3' sequence available.
 This clone (DKFZ31300939) is available at the RZPD in Berlin.
 Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 Berlin-Charlottenburg, Germany; Email: clone@rzpd.de.
 Location/Qualifiers
 FEATURES
 SOURCE 1..758
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="DKFZ31300939"
 /clone_id="313 (synonym: hlcc2)"
 /dev_stage="adult"
 /lab_host="DH10B"
 /note="Vector: pT7-19x2; Site_1: SfiIA; Site_2: SfiIB; cDNA-collection"

BASE COUNT 167 a 231 c 211 g 145 t 4 others
 ORIGIN

alignment_scores:
 Quality: 804.50 Length: 173
 Ratio: 4.905 Gaps: 1
 Percent Similarity: 94.798 Percent Identity: 91.329

alignment_block:
 US-09-762-491-6 x AL601137 ..

Align seg 1/1 to: AL601137 from: 1 to: 758

```

1 MetSerCyAllylsuEtrProSerGlyAlaProAlaProLeuValSe 17
|||||
192 ATCTCTGCGCTCAAGTTATGCGCCAGCGCTGCGCCCTTCGCTC 241
|||||
17 TTAGGUGUUGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGUAGU 34
|||||
242 CATCGAGAACTGAGAACCAAGACCTGCTGCGAAAGCGGTTGCGCA 291
|||||
34 hVAlPheArGAlaGlnHlaArGlySTrPGlyTYrAspValAlaValLys 50
|||||
292 CAGTGTTCGGGGCGCAATAGGAAGTGGGCTACGATGTCGGGTCAG 341
|||||
51 lLeValAsnSerLysAlaIleSerArgLysValLysAlaMetAlaSerLe 67
|||||
342 ATGCTAACTCGAAGCGCATATCGAGGAGTCAAGCCATCGCAACTC 391
|||||
67 uAspAaGluPheValLeuArGLeuGlyValIleGluLysValAsnT 84
|||||
392 GGTAAAGCAATTCGTGCTGCGCTAGAGGGGTTATGAGAAAGGTCAACT 441
|||||
84 tPAspGlnAspProLysProAlaLeuValIThrLysPheMetGluAsnGly 100
|||||
442 GGGACCAAGATCCCAAGCGGCTGTGTGACTAAATTCAATGAGAAAGCGG 491
|||||
101 SerLeuSerGlyLeuLeuGlnSerGlnCyProArgProTrpProLeu 117
|||||
492 TCCCTTTCGGGGCTGCGAAGTCCAGATGCGCCCTGCGGCTCCCT 541
|||||
117 uCyAaGLeuLeuLysGluValValLeuGlyMetPheTyrLeuHlaAsp 134
|||||
542 TTGCCCCCTGCTGAAAGAGTGTGCTGGGATGTTTACCTCGACAGACC 591
|||||

```

134 lAsnProValLeuLeuHlaArGAspLeuLysProSerAsnValLeuPro 150
 |||||
 592 AAGACCGGCTCTCTGACCGGAGACCTCAAGCCATCGACGCTGCGG 641
 |||||
 151 AspProGluLeuHlaValLysLeuAlaAspPheGlyLeuSerThrPheLe 167
 |||||
 642 GACCGACGCTGACGTCAGAGTCACG.....TCGTCACACCCCT 682
 |||||
 167 nGlyLysSerGlnSerGly 173
 |||||
 683 CTCACGCTCAAGCAAGCC 701
 |||||

seq_name: gb_est2:BI905455

seq_documentation_block:
 LOCUS BI905455 906 bp mRNA linear EST 16-OCT-2001
 DEFINITION 603167947F1 NCI-CGAP_Lu33 Mus musculus cDNA clone IMAGE:5256010 5',
 mRNA sequence.
 ACCESSION BI905455
 VERSION BI905455.1 GI:16167978
 KEYWORDS EST.
 SOURCE house mouse.
 ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 906)
 AUTHORS NIH-MGC http://mgc.nci.nih.gov/
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cga@bbs-rtmail.nih.gov
 Tissue Procurement: Gilbert Smith, Ph.D.
 cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo, Ph.D.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LMNL)
 cDNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LMNL at:
 http://image.llnl.gov
 plates: LMNL1646 row: n column: 11
 High quality sequence start: 807.
 High quality sequence stop: 807.
 Location/Qualifiers
 FEATURES
 SOURCE 1..906
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone_image="5256010"
 /clone_id="NCI-CGAP_Lu33"
 /tissue_type="pooled lung tumors"
 /lab_host="DH10B (phage-resistant)"
 /note="Organ: lung; Vector: pT7-3D-Pac (Pharmacia) with a modified polylinker; Site_1: NotI; Site_2: EcoRI; 1st strand cDNA was prepared from mRNA obtained from pooled lung tumors with a Not I - oligo(dT) primer [5' TGTTACCAATCTGAATGAGACGCGCCCTCTTTTCTTTTCTTTT 3']
 Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7-3D vector. Library went through one round of normalization, and was constructed by Bento Soares and M. Fatima Bonaldo."

BASE COUNT 188 a 245 c 265 g 208 t

alignment_scores:
 Quality: 780.50 Length: 231
 Ratio: 3.771 Gaps: 5
 Percent Similarity: 82.470 Percent Identity: 70.120

alignment_block:
 US-09-762-491-6 x BI905455 ..

Align seg 1/1 to: B1905455 from: 1 to: 906

[illegible]

Seq_name: gcb_est2:BI833736

seq_documentation_block:

LOCUS	BI837336	616 bp	mRNA	linear	EST 04-OCT-2001
DEFINITION	603086473F1 NIH_MGC_120	Homo sapiens	CDNA	clone IMAGE:5227291	5'

ACCESSION PT033736

VERSION BI833736.1 GI:15945286

KEYWORDS EST.
SOURCE human.

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Euthera; Primates; Catarrhini; Hominoidea; Homo.

REFERENCE

1 (bases 1 to 616)

AUTHORS
TITLE

NIH-MGC <http://mgc.ncl.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)

COMMENT

Contact: Robert Strausberg, Ph.D

Email: cgapbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrived by: The I. M. A. G. E. Consortium (IMT)

DNA Sequencing by: Incyte Genomics, Inc.

found through the I.M.A.G.E. Com-

FEATURES

Location/Qualifiers
1. .616

```
/organism="Homo sapiens"  
/db_xref="taxon:9606"
```

```

/clone="IMAGE:5227291"
/clone lib="NTH MGC 120"

```

/note:organ: pooled pancreas and spleen; Vector: pCMV-Sport6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA source anonymous pool of spleen and pancreas from 28 yo male. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.5 kb, insert size range 1-2.5 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 025. Note: this is a NTR/MGC Library.

US-09-762-491-6 x BI833736

Align seg 1/1 to: BI833736 from: 1 to: 616

1 MetSerCysValLysValLeuTPRPProSGlyAlaProAlaProLeuValSe 17
162 ATTCGTGTCGTCAGATTATGGCCACGCGTCCCCCCCCCTTGGTGTG 211
17 rLlGluGluLeuGluAnGluInGluLeuValGlyLysAspGlyPheGlyLT 34
212 CATCCGCGAGCACTGGAGAACCGAGAGCTGTCGGCAAGGCGGGTTGGCA 261
34 hcrValPheArCAlGlnHLSrGlySTPGLYTcrAspValAlaValLys 50
262 CAGTCTTCCGGGCCCAACrAGAAACTGGGGCTACGATGGCGGTGTCAAG 311
51 lIeValAnSerLysValAlaIleSerArgLysValLysAlaMetAlaSerIle 67
312 ATGTGAACTGGAAGGCGATTCACGGGAGGTGTCAAGCCATGGCAAGTCT 361
67 uAspAnGluPheValLeuArgLeuGluGlyValIleGluLysValLAsnT 84
162 GGATTAACGAAATTCGTGGTGGCTGAAAGGGGTTATCGGAAGAAGTGA 411
84 rPAspGluAspProLysProAlaLeuValITrPAspPheMetGluuAsnGly 100
412 GGAGCAAGATCCCAACGCGGCTGGTGGACTAAATTCAACGAGAACGGC 461
101 SerLeuSerGlyLeuLeuGlnSerGlnCysProArgProTrpProLeuLe 117

```

|||||
462 TCCCTGGGGGCTGCTCCAGTCCCTGCGCCCTGCGCTCT 511
117 UCyAaGLeuLeuLysGluValValLeuGlyMetPheTyrLeuHisAspG 134
512 TTGCGCGCTCTCTGAAGAAGTGGTCTTGAGATTTTACCTGCACGACC 561
134 LnaaNPoVallLeuLysAspLeuLysProSerAsnValLeuPro 150
562 AGAACCGGTCCTGTCACCGGAGCTCAACCATCCACGCTCTGCTG 611
151 Asp 151
612 GAC 614

seq_name: gb-est1:AA227673
seq_documentation_block: 440 bp mRNA linear EST 06-AUG-1997
LOCUS AA227673
DEFINITION z55d09.r1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:667313
5' mRNA sequence.
ACCESSION AA227673
VERSION AA227673.1 GI:1849253
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homindae; Homo.
1 (bases 1 to 440)
Hillier, L., Allen, M., Bowles, L., Dubuque, T., Gelsel, G., Jost, S.,
Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B.,
Schellenberg, R., Stepien, M., Tan, F., Thelasing, B., White, Y., Wylie,
T., Watson, R. and Wilson, R.
WashU-Merck EST Project 1997
Unpublished (1997)
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LUML; contact the
IMAGE Consortium (info@image.lum.gov) for further information.
Insert length: 829 Std Error: 0.00
Seq primer: 28m13 rev7 ET from Amer sham.
Location/Qualifiers
FEATURES
Source
1. 440
/organism="Homo sapiens"
/db_xref="Gene:5561280"
/db_xref="taxon:9606"
/clone="IMAGE:667313"
/clone_1kb="Soares_NHMPu_S1"
/lisase_type="Pooled human melanocyte, fetal heart, and
pregnant uterus"
/jab_host="DH108"
/Note="Organ: mixed (see below); Vector: p7773D-Pac
(Pharmacia) with a modified polylinker; Site: 1: Not 1;
Site 2: Eco RI; Equal amounts of plasmid DNA from three
normalized libraries (melanocyte 2NDM, pregnant uterus
NDMPu, and fetal heart NDH1W) were mixed, and 88 clones
were made in vitro. Following NAR purification, this DNA
was used as tracer in a subtractive hybridization
reaction. The driver was PCR-amplified cDNAs from pools of
5,000 clones made from the same 3 libraries. The pools
consisted of I.M.A.G.E. clones 260232-265223,
340488-345479, and 468488-489479."
BASE COUNT 131 a - 119 c 111 g 79 t
ORIGIN

```

alignment_scores:
 Quality: 760.00 Length: 145
 Ratio: 5.278 Gaps: 0

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Percent Similarity: 99.310 Percent Identity: 99.310
alignment_block:
US-09-762-491-6 x AA227673 ..
Align seg 1/1 to: AA227673 from: 1 to: 440

315 pHeaSerIleProGluSerGlyGlnGlyGlyThrGluMetAspGlyPheAr 331
5 TTTTATATCCAGACTCAGGCCAAGAGGAGCAAGAAATGATGATGGCTTAG 54
331 gArGThrIleGluAngIHisSerArgAsnAspValMetValSerGluT 348
55 GAGAACATATAGAAAACAGCAGCTCTGATATGATCTCATGTTCGTGAGT 104
348 rPLeuAsnLysLeuAsnLeuGluGluProProSerSerValProLysLys 364
105 GGCTAAACAAACTGATCTAGAGAGAGCTCCAGCTCTGTCTCTAAAAAA 154
365 cysProSerLeuThrLysArgSerArgAlaGlnGluGlnGluValProG 381
155 TCCCGAGCCCTTACCAAGAGAGAGAGGA.CAAGAGAGAGAGGTTCCACA 203
381 nAlaTrpThrAlaGlyThrSerSerAspSerMetAlaInProGlnTr 398
204 ACCTGGACAGCAGCAGCAGCATCTTCAGATTGATGCGCCCACTCCAGCA 253
398 hPrGluThrSerThrPheArgAsnGlnMetProSerProThrSerThr 414
254 CTCACAGACCTCAACTTCAGAAACAGACATCCAGCCCTCACTCACT 303
415 GlyThrProSerProGlyProArgGlyAsnGlnGlyAlaGluArgGln 431
304 GGAACACCAAGTCTGGAGCCCGAGGATACAGGGGCTGAGAGACAGG 353
431 yNeaAsnTrpSerCysArgThrProGluProAsnProValThrGlyArg 448
354 CATGACGCTCTGTCAGAGACTCGGAGCCAAATCCAGTAACAGAGCAG 403
448 rOLeUValAsnIleTyrAsnCysSerGlyValGln 459
404 CGCTGTTAACTATACAACTGCTCGGGGTGCAM 438

seq_name: gb-est1:AW106218
seq_documentation_block: 821 bp mRNA linear EST 20-OCT-1999
LOCUS AW106218
DEFINITION um24g06.y1 Sugano mouse embryo meva Mus musculus cDNA clone
IMAGE:2225530 5' similar to TR:0922P5 Q922P5 HOMOXYSTRINE
RESPONDENT PROTEIN HCYP2. ; mRNA sequence.
ACCESSION AW106218
VERSION AW106218.1 GI:6076954
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 821)
REFERENCE
1 Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T.,
Marra, M., Allen, M., Bowles, L., Lennon, G., Moore, B.,
Schellenberg, R., Stepien, M., Tan, F., Thelasing, B., White, Y.,
Wylie, T., Watson, R., Stepien, M., Tan, F., Thelasing, B., White, Y.,
Wylie, T., Watson, R. and Wilson, R.
WashU-Merck EST Project 1999
Unpublished (1999)
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LUML; contact the

```

IMAGE Consortium (info@image.llnl.gov) for further information.
 MG:1005726

Seq primer: custom primer used
 High quality sequence stop: 517.
 Location/Qualifiers

FEATURES

source

1. 821
 /organism="Mus musculus"
 /strain="C57BL"
 /db_xref="taxon:10090"
 /clone_image="2225350"
 /clone_id="Sugano mouse embryo mewa"
 /dev_stage="embryo, 14 dpc"
 /lab_host="DH10b"
 /note="Vector: pME18S-FL3; site_1: DraIII (CACTGTGTG); site_2: DraIII (CACCATGTG); 1st strand cDNA was primed with an oligo(dT) primer (ATGGGCGCTTTTCTTTTCTTTT); double-stranded cDNA was ligated to a DraIII adaptor (TCTGGCGCTTGTG); digested and cloned into distinct DraIII sites of the pME18S-FL3 vector (5' site CACTGTGTG, 3' site CACCATGTG). XhoI should be used to isolate the cDNA insert. Size selection was performed to exclude fragments <1.5kb. Library constructed by Dr. Sumio Sugano (University of Tokyo Institute of Medical Science). Custom primers for sequencing: 5' end primer CTTCTGCTTAAAGCTGCG and 3' end primer CGACCTGACGCTCGACACA."

BASE COUNT 171 a 223 c 239 g 185 t 3 others
 ORIGIN

alignment_scores:
 quality: 698.50 length: 213
 ratio: 4.085 gaps: 2
 Percent Similarity: 80.282 Percent Identity: 68.075

alignment_block:
 us-09-762-491-6 x AW106218 ..

Align seg 1/1 to: AW106218 from: 1 to: 821

```

1 MetSerCyValIyLeuTrpProSerGlyAlaProAla...ProLeuVa 16
||||| ||||||| ||||||| ||||||| ||| |||||||
183 ATGCTCTCTCTCAACTATGCGCTGCTGCTGACGCGCTTCTCTGCG 222
16 IserIleGluIleGluAsnGluIleuValGlyIyAsnPolyphed 33
||||| ||||||| ||||||| ||||||| |||||||
233 GAGCGCGAAGAACCTGAAAGCTGTGCTGTGCTAAAGAGGCTTC 282
33 IythrValIphearGAlaGlnHisArgIySTrpgIyTyrAspValAlaVal 49
||||| ||||||| ||||||| ||||||| |||||||
283 GAGCGCTGCTCGCGCACACACACACATGACGACGATGACGACGTC 332
50 LyAlIeValIAsnSerIyAlaIleSerArgIuValIyAlaMelaIase 66
||||| ||||||| ||||||| ||||||| |||||||
333 AAGATCTGTAACCTGAAAGACATATCTGCGGCGTGAAGGCTATGTTAA 382
66 rLeuAspAsnGluPheValIleuArgIleuGluIyValIleGluIyValA 83
||||| ||||||| ||| ||| ||| ||| ||| ||| ||| ||| |||
383 TCTTCGTAATGAGAACGTTCTCTCTCTCTGCGGCTCTGACGACCTTC 432
83 entrAspAsnProIySProAlaIleuValIThrIySPhemeGluAsn 99
||||| ||||||| ||||||| ||||||| |||||||
433 AGTGAGACTTCTGTCGCGGACGCTGTGCTGACAAAGTTCATGAGAAAT 482
100 GlySerLeuAsnSerGlyLeuLeuGlnSerGlnGlyProArgProTyrPro 116
||||| ||||||| ||||||| ||||||| |||||||
483 GCGTCCCTCTAGCGCTCTGACACCGACGTCGCGCGCTCTGCGCACAT 532
116 uLeuCyArgIleuIleuValIyAlaIleuGlyIyMetPheTyrLeuAla 133
||||| ||||||| ||||||| ||||||| |||||||
533 CCTGTGTGCGCTCTCTGACGAGAGTGTCTGCGGATGTGCTACTACACA 582
133 spoinAsnProValIleuLeuHisArgAspLeuIySProSerAsnValIleu 149

```

```

||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
583 GATTCAACCTCCCTCTCTGACCGGACCTCAAGCCCTCTTAACATTCGTG 632
150 ProAspProGluLeuHisValIyLeuAlaAspPheGlyLeuSerThrph 166
||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
633 CTGATTCACAGAGCTTACGCGCAAGCTAGACGATATGCGCTGTACGTT 682
166 eGlnGlyIySerGlnSerGlyThrIySerGly.....Glyp 179
||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
683 TCAAGAGAGGCGCCAGTCAGGCTGACGATGACGATCAGGATCCAGGACT 732
179 roGlyIyThrIleGlyIyLeuAlaProGluLeuPheValAsnValAsn 195
||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
733 CTGGGCGCACCCCTAGCTACTTGTGACCCCAAGCTGTATGTGATGTAAAC 782
196 ArgIyAlaSerThrAlaSerAspValIySerPheGly 208
||||| ||||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
783 CTGAAGGCTCTTAAGCAGAGATGTCTACAGCCTTTGCA 821

```

seq_name: gb_esc2:B1985826

seq_documentation_block:

LOCUS B1985826 600 bp mRNA linear EST 20-DEC-2001
 DEFINITION 3152-49 Mouse E14.5 retina lambda ZAP II library Mus musculus cDNA,
 mRNA sequence.
 ACCESSION B1985826
 VERSION B1985826.1 GI:17956767
 KEYWORDS EST.

SOURCE house mouse.

ORGANISM

Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

REFERENCE

1 (Bases 1 to 600)
 White,R.A., Beremand,P.D., Thomas,T.L., Gen.L. and Klein,M.H.
 Gene expression in the developing mouse retina by EST sequencing
 and microarray analysis
 Nucleic Acids Res. 29 (24), 4983-4993 (2001)

JOURNAL

Contact: Klein WH
 Department of Biochemistry and Molecular Biology
 University of Texas M.D. Anderson Cancer Center
 Box 117, 1515 Holcombe Blvd., Houston, TX 77030, USA
 Tel: 713 792 3646
 Fax: 713 790 0329.

FEATURES Location/Qualifiers

SOURCE

1. 600
 /organism="Mus musculus"
 /db_xref="taxon:10090"
 /clone_id="Mouse E14.5 retina lambda ZAP II library"
 /tissue_type="neural retina"
 /dev_stage="embryonic day 14.5 post-fertilization"
 BASE COUNT 123 a 165 c 178 g 133 t 1 others
 ORIGIN

alignment_scores:
 quality: 693.00 length: 200
 ratio: 4.175 gaps: 2
 Percent Similarity: 83.000 Percent Identity: 71.000

alignment_block:
 us-09-762-491-6 x B1985826 ..

Align seg 1/1 to: B1985826 from: 1 to: 600

```

67 LeuAspAsnGluPheValIleuArgIleuGluIyValIleGluIyValAs 83
||||| ||||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
3 CTTCGTATGAGAACGTTCTGCTGCTGCGGCGTCACTGAGAGACCTCCA 52
83 nTrAspGlnAspProIySProAlaIleuValIThrIySPhemeIleuAsn 100
||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
53 GTGGACTTCTGTGCGGCGAGGCTGTGCTGACAAAGATTCATGAGAAATG 102

```

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100  lySerLeuSerGlyLeuLeuGlnSerGlnGlyProAlaGlyProThrProLeu 116
101  |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
102  103  GGTCCCTGCAAGGCTGCTGCACCCGCAAGTCCCTGCGCCCTGCACAC 152
104  117  LeuGlyAlaGlyLeuLeuGlyGlyValValLeuGlnLysMetPheThrLeuHis 133
105  |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
106  153  CTCTGTTCGCTGTCTCAGGAAGATGCTGTGGGTGTGCTACTCTACACAG 202
107  133  pGlnAsnProValLeuLeuHisArgAspLeuLysProSerAsnValLeuP 150
108  |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
109  203  CTTGAACCTTCCGCTCTGCACCCGGGACCTCAAGCCCTTCAACATTCTGC 252
110  150  roAspProGlyLeuHisValLysLeuAlaAspPheGlyLeuSerThrPhe 166
111  |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
112  253  TCGATCTCAGAGCTCCACGCCAAGTACAGATTGTGCGCTGTCCAGGTTT 302
113  167  GlnGlyGlySerGlnSerGlyThrGlySerGly.....GluPr 179
114  |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
115  303  CAGGGAGGGTCCCATCAGGTCAAGGTCAAGATCAAGATCAAGGACATC 352
116  179  oGlyGlyThrLeuGlyTyrLeuAlaProGlyLeuPheValAsnValAsna 196
117  |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
118  353  TCGGGGCAACCTAGCGTACTTGGACCCGAGAGCTCTTATTGGATGTCACAC 402
119  196  rgLysAlaSerThrAlaSerAspValTyrSerPheGlyLysLeuMetPr 212
120  |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
121  403  TGAAGGCTTCTAAAGCGAGTGATGTCTACACACTTTGGGATCCCTCGGTGG 452
122  213  AlaValLeuAlaGlyTyrGlyValGluLeuProThrGluProSerLeuY 229
123  |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
124  453  GGAGTGCTGGCTGGCAGAGAAAGCTGACTTTGGTAGACAACACTTCACTAA 502
125  229  aTyrGluAlaValAlaCysAsnArgGlnAsnArgProSerLeuAlaGluLeu 245
126  |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
127  503  TCCCGGCAAACTGTGTACACAGCAGAGTGTCTCTCACTACAGACAGCTG 552
128  246  ProGlnAlaGlyProGlyThrPheGlyLeuGlnGlyLysLeuGlyLeu 261
129  |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
130  553  CCTCCAGGAGCCCTGAGACTCTCCGGCTTGGAAAACCTGAAGAGATT 600

```

Thu Aug 15 09:40:55 2002

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178 uproglgltgthleuglttyrlemlaProclenu..... Phaya 193
    |||||:::|||||:::
691 ctctggggggacacctgacgcgtacttgggccccaagacctgcatttAAA 740
193 anvalaanaagysalasetrlnlaseraapvaltyser.Phegy11 209
    |||||:::|||||:::|||||:::
741 gtcaaccttaaaagccgtcttAAAGCAGtGtGTCTACAGCATTGGGAT 750
209 eleumettPala 213
    |||||:::|||||
791 cctctgtgtggGCC 803

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ACCESSION	BF359285				
VERSION	BF359285.1	GI:11318461			
KEYWORDS	EST.				
SOURCE	human.				

REFERENCES

TITLE	Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MENT ID#	20207663

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE 20202663
COMMENT Contact: Simpson A.J.G.

COMMENT

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Brazil
Tel.: +55-11-2704832
Fax: +55-11-2707001
Email: aslmpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
<http://www.ludwig.org.br/scripts/gethtml2.pl?tl=RC6&t=RC6-ET0081>
100700-012-B10&t3=2000-07-10&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 36
High quality sequence stop: 367.

FEATURES
source

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/organism="Homo sapiens"
/db_xref="taxon:9606"
/cclone.lib="ET0081"
/dev_stage="Adult"
/notes="Organ: lung_tumor; Vector: puc18; Site:1: SmaI; Site:2: SmaI; Ampli.Library was made by cloning products derived from ORESTAS PCR (U.S. Letters Patent Application No. 196,716 - Ludwig Institute for Cancer Research) Profiles 176 - The pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
BASE COUNT      88 a      143 c      109 g      90 t      2 others
ORIGIN

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  Ratio: 5.178        Gaps: 0
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alignment block:
US-09-762-491-6 x BF359285/rev ..
Align seg 1/1 to reverse of: BF359285 from: 1 to: 432

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1 mEtScCySvAlLySvLsEuRPrProSeCjLyAlaProLeValSe 17
423 ATGTGCTGGTCACAAAGTTATGGGCCACGGGTCCACCGCCACCTTGGTGTC 37
17 rTlEGuGluBuEuGluuAnGInGluLeuValGlyLyAspGlyPhGcLyT 34
373 CATCGAGAACCTGAGAACCAAGAGACTCGTCTGGCAAAAGCGGGGTTCGGCA 324
34 hVvAlPhaTrAlAlGInHlSAuGlyTrpGlyTrpAspAlaValLys 50
323 CAGTGTCTCGGGCCCAACATAGAAAGTGGGGCTACGATGGGGGTCAAG 274
51 iLeValAsnSerLySaIaIeSerArgLyuValLysAlaMetAlSeRle 67
273 ATCTGTAACCTGAAAGCGGATATCCAGGAGGTCAAGCCATGGCAAGTCT 224
67 uAphAnGluPhEuValLeuArgLeuGluGlyValIleGluLyvAlaLeuT 84
223 GGAATACCAATTCCTGTGGCTCGAAAGGGGTATCGAAAGGTGAACCT 174
84 rPAspGluAspProLySProAlaLeuValIThrLySPhenGtLuAnGly 106
173 GGGACCAAGATCCCAAGCCGGCTCTGGTGACTAATTCATGGAGAACGGC 124
101 SerLeuSerGlyLeuGluGlnSerGlnAspProArgProTrpProLeu 117
123 TCCCTGTGGGGCCGCGCTGACAGTCCACAGTCCCTCGAGCCGCCCTCTCT 74
117 uCyArGluLeuLysGluValValLeuGlyMetPheTyTLeuHlAsp 133
73 TrCGCGCTGTGAAGAAAGTGGTCTCTGGAGATTTTAACTGCAAGAC 25